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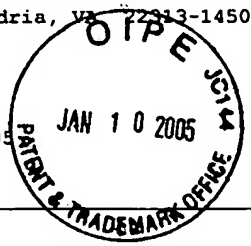

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PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Group: 1645

Jie Chen, et al.

Serial No.: 10/733,969

Filed: December 11, 2003

For: **SPECIFIC MARKERS FOR PANCREATIC CANCER**

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Dear Sir:

Attached please find two certified copies of the foreign application from which priority is claimed for this case:

Country	Application No.	Filing Date
Europe	02028058.2	December 17, 2002
Europe	03025237.3	November 5, 2003

Respectfully submitted,

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Bescheinigung | Certificate | Attestation

Die angehefteten Unterlagen stimmen mit der ursprünglich eingereichten Fassung der auf dem nächsten Blatt bezeichneten europäischen Patentanmeldung überein.

The attached documents are exact copies of the European patent application described on the following page, as originally filed.

Les documents fixés à cette attestation sont conformes à la version initialement déposée de la demande de brevet européen spécifiée à la page suivante.

Patentanmeldung Nr. | Patent application No. | Demande de brevet n°

02028058.2

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
p.o.

R C van Dijk

Anmeldung Nr:
Application no.: 02028058.2
Demande no:

Anmeldetag:
Date of filing: 17.12.02
Date de dépôt:

Anmelder/Applicant(s)/Demandeur(s):

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SUISSE

Bezeichnung der Erfindung/Title of the invention/Titre de l'invention:
(Falls die Bezeichnung der Erfindung nicht angegeben ist, siehe Beschreibung.
If no title is shown please refer to the description.
Si aucun titre n'est indiqué se referer à la description.)

Specific markers for pancreatic cancer

In Anspruch genommene Priorität(en) / Priority(ies) claimed /Priorité(s) revendiquée(s)
Staat/Tag/Aktenzeichen/State/Date/File no./Pays/Date/Numéro de dépôt:

Internationale Patentklassifikation/International Patent Classification/
Classification internationale des brevets:

C12Q/

Am Anmeldetag benannte Vertragstaaten/Contracting states designated at date of filing/Etats contractants désignées lors du dépôt:

AT BE BG CH CY CZ DE DK EE ES FI FR GB GR IE IT LI LU MC NL PT SE SI SK

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Case 21525

SPECIFIC MARKERS FOR PANCREATIC CANCER

The present invention relates to markers for diagnosis of pancreatic cancer comprising at least one polypeptide identified by proteomics to be up-regulated in pancreatic cancer, to an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of specific markers as disclosed herein. Furthermore, screening methods relating to antagonists of the specific markers disclosed herein are provided.

Background

Pancreatic cancer is a common cause of death in the Western world. It is one of the most aggressive malignant tumors, with an overall 5-year survival rate of 0.4%. In many patients with pancreatic cancer, accurate preoperative diagnosis is difficult to achieve with conventional imaging analyses. Most patients with pancreatic cancer present late in the course of the disease and have either locally extensive or metastatic disease. Overall, only up to 20% are candidates for resection and have the potential for curative surgery. Among the causes for this late presentation is the lack of diagnostic methods for an earlier detection of the disease. Besides this lack of diagnostic methods, the high mortality of patients with pancreatic cancer is additionally caused by a lack of effective treatments. Therefore, the identification of new targets for early diagnosis of pancreatic tumors, and for the development of agents to treat pancreatic cancer is a challenge of paramount importance.

Detailed Description of the Invention

The problem of identifying polypeptides suitable as markers of pancreatic cancer for early diagnosis of the disease, and the long felt need for such markers, was overcome by the present invention by applying the new technology of proteomics. It was surprisingly found by using proteomic technology that a specific set of polypeptides are differentially expressed in pancreatic tissue obtained from individuals suffering from pancreatic cancer, as compared to healthy pancreatic tissue. Said differentially expressed polypeptides are listed in appended tables 2 and 3. The polypeptides in table 3 are encoded by genes which were previously identified to be up-regulated in pancreatic cancer on the transcriptional level (Iacobuzio-Donahue et al., (2002), Am. J. Pathol. 160, 1239-1249). However, it is well known that regulation on the transcriptional level is not necessarily indicative of a similar regulation of the expression of the respective gene on the translational level. Thus, only by demonstrating that the polypeptides listed in table 3 are up-regulated in pancreatic cancer is it possible to use them for polypeptide-based diagnostic assays for the detection of pancreatic cancer.

Based on the polypeptides listed in tables 2 and 3, the present invention provides a marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3 (Seq ID No. 1 to 24 and 26 to 49; and/or Seq ID No. 25 and 50 to 55). Thus, the term "marker" as used herein refers to one or more polypeptides that are regulated in cancer and that can be used to diagnose pancreatic cancer or a susceptibility to pancreatic cancer either alone or as combinations of multiple polypeptides that are known to be regulated in pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48; and/or Seq ID No. 25 and 50 to 54. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15, 27, 31 to 35, 37, 39, 40; and/or Seq ID No. 50 to 52. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 and/or Seq ID no. 51 and 52. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15, and 31; and/or Seq ID No. 52.

The term "polypeptide" as used herein, refers to a polymer of amino acids, and not to a specific length. Thus, peptides, oligopeptides and proteins are included within the definition of polypeptide.

Preferably, the marker of this invention is a marker comprising at least one polypeptide selected from the group consisting of the polypeptides listed in table 2.

Furthermore, a polypeptide selected from the group consisting of the polypeptides listed in tables 2 and/or 3, is used as a marker or as part of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer. Preferably, said polypeptides are selected from the group consisting of Seq. ID No. 2 to 10, 12 to 15, 17, 19, 20, 23, 24, 27, 28, 31 to 40, 42 to 45, 47 and 48 from table 2 and/or Seq ID No. 25 and 50 to 54 from table 3. These polypeptides are induced at least two fold, as can be seen in tables 2 and 3. More preferably, said polypeptides are selected from the group consisting of Seq ID No. 3, 4, 6, 9, 14, 15 ,27, 31 to 35, 37, 39, 40 from table 2 and/or Seq ID No. 50 to 52 from table 3. These polypeptides are induced at least three fold, as can be seen in tables 2 and 3. Even more preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 9, 14, 15, 31, 33 to 35 from table 2 and/or Seq ID No. 51 and 52 from table 3. These polypeptides are induced at least 4 fold, as can be seen in tables 2 and 3. Most preferably, said polypeptides are selected from the group consisting of Seq ID No. 4, 6, 14, 15 and 31 from table 2 and/or Seq ID No. 52 from table 3, which are the polypeptides that are induced five fold, as shown in tables 2 and 3.

With the identification of polypeptides regulated in pancreatic cancer, the present invention provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of obtaining a biological sample; and detecting and/or measuring the increase of a marker described hereinbefore. The term "detection" as used herein refers to the qualitative determination of the absence or presence of polypeptides. The term "measured" as used herein refers to the quantitative determination of the differences in expression of polypeptides in biological samples from patients with pancreatic cancer and biological samples from healthy individuals. Methods

for detection and/or measurement of polypeptides in biological samples are well known in the art and include, but are not limited to, Western-blotting, ELISAs or RIAs . Antibodies recognizing the polypeptides listed in tables 2 and/or 3 can either be generated for the purpose of detecting said polypeptides, eg. by immunizing rabbits with purified proteins, or known antibodies recognizing said polypeptides can be used. For example, an antibody capable of binding to the denatured proteins, such as a polyclonal antibody, can be used to detect the peptides of this invention in a Western Blot. An example for a method to measure a marker is an ELISA. This type of protein quantitation is based on an antibody capable of capturing a specifc antigen, and a second antibody capable of detecting the captured antigen. A further method for the detection of a diagnostic marker for pancreatic cancer is by analysing biopsy specimens for the presence or absence of the markers of this invention. Methods for the detection of these markers are well known in the art and include, but are not limited to, immunohistochemistry or immunofluorescent detection of the presence or absence of the polypeptides of the marker of this invention. Methods for preparation and use of antibodies, and the assays mentioned hereinbefore are described in Harlow, E. and Lane, D. Antibodies: A Laboratory Manual, (1988), Cold Spring Harbor Laboratory Press.

The accuracy of the diagnosis of pancreatic cancer can be increased by analysing combinations of multiple polypeptides listed in tables 2 and/or 3. Thus, the in vitro method herein before described, comprises a marker which comprises at least two, preferably at least three, more preferably at least four, even more preferably at least five, and most preferably at least six of the polypeptides listed in tables 2 and/or 3.

For diagnosis of pancreatic cancer, suitable biological samples need to be analysed for the presence or absence of a marker. Said biological samples can be serum, plasma, pancreatic juice or cells of pancreatic tissue. Cells from pancreatic tissue can be obtained by ERCP, secretin stimulation, fine-needle aspiration, cytologic brushings and large-bore needle biopsy.

It is also possible to diagnose pancreatic cancer by detecting and/or measuring nucleic acid molecules coding for the marker hereinbefore described. Preferably, said nucleic acid molecule is RNA or DNA. In another embodiment, said DNA is a cDNA.

In one embodiment of the present invention, the in vitro method herein before described comprises comparing the expression levels of at least two of the nucleic acids encoding said polypeptides in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer, to the expression levels of the same nucleic acids in a healthy individual.

In another embodiment of the present invention the in vitro method herein before described comprises comparing the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer to the expression levels of the same marker in a healthy individual. In a more preferred embodiment of the in vitro method, an increase or decrease of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

The present invention also provides a screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and detecting the interaction between said compound or plurality of compounds with said polypeptide.

The "interaction" in the screening methods as disclosed herein may be measured by conventional methods. The type of conventional method for testing the interaction of a compound with a polypeptide that is soluble, as opposed to membrane associated, can be an in vitro method using either purified recombinant polypeptide, or native polypeptide purified from cells that endogenously express the polypeptide. As a non-limiting example, a polypeptide of the invention can be bound to beads or immobilized on plastic or other surfaces, and interaction of a compound with the polypeptide can be measured by either using a labelled compound and measuring the label bound to the polypeptide, or by displacement of a labeled known ligand from said polypeptide.

For polypeptides that are associated with the cell membrane on the cell surface, or which are expressed as transmembrane or integral membrane polypeptides, the interaction of a compound with said polypeptides can be detected with different methods which include, but are not limited to, methods using cells that either normally express the polypeptide or in which the polypeptide is overexpressed, eg. by detecting displacement of a known ligand which is labeled by the compound to be screened. Alternatively, membrane perparations may be used to test for interaction of a compound with such a polypeptide

Interaction assays to be employed in the method disclosed herein may comprise FRET-assays (fluorescence resonance energy transfer; as described, inter alia, in Ng, Science 283 (1999), 2085-2089 or Ubarretxena-Belandia, Biochem. 38 (1999), 7398-7405), TR-FRETs and biochemical assays as disclosed herein. Furthermore, commercial assays like "Amplified Luminescent Proximity Homogenous Assay™" (BioSignal Packard) may be employed. Further methods are well known in the art and, inter alia, described in Fernandez, Curr. Opin. Chem. Biol. 2 (1998), 547-603.

The "test for interaction" may also be carried out by specific immunological and/or biochemical assays which are well known in the art and which comprise, e.g., homogenous and heterogenous assays as described herein below. Said interaction assays employing read-out systems are well known in the art and comprise, inter alia, two-hybrid screenings (as, described, inter alia, in EP-0 963 376, WO 98/25947, WO 00/02911; and as exemplified in the appended examples), GST-pull-down columns, co-precipitation assays from cell extracts as described, inter alia, in Kasus-Jacobi, Oncogene 19 (2000), 2052-2059, "interaction-trap" systems (as described, inter alia, in US 6,004,746) expression cloning (e.g. lamda gt11), phage display (as described, inter alia, in US 5,541,109), in vitro binding assays and the like. Further interaction assay methods and corresponding read out systems are, inter alia, described in US 5,525,490, WO 99/51741, WO 00/17221, WO 00/14271 or WO 00/05410. Vidal and Legrain (1999) in Nucleic Acids Research 27, 919-929 describe, review and summarize further interaction assays known in the art which may be employed in accordance with the present invention.

Homogeneous (interaction) assays comprise assays wherein the binding partners remain in solution and comprise assays, like agglutination assays. Heterogeneous assays comprise assays like, inter alia, immuno assays, for example, Enzyme Linked Immunosorbent Assays (ELISA), Radioactive Immunoassays (RIA), Immuno Radiometric Assays (IRMA), Flow Injection Analysis (FIA), Flow Activated Cell Sorting (FACS), Chemiluminescent Immuno Assays (CLIA) or Electrogenerated Chemiluminescent (ECL) reporting.

The present invention further provides a screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in table 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting said polypeptide with a compound identified and/or obtained by the screening method described above under conditions which allow interaction of said compound with said polypeptide; b) determining the activity of said polypeptide; c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist. The terms inhibitors and antagonists as used herein are used interchangeably. This screening assay can be performed either as an in vitro assay, or as a host-based assay. The host to be employed in the screening methods of the present invention and comprising and/or expressing a polypeptide listed in tables 2 and/or 3 may comprise prokaryotic as well as eukaryotic cells. Said cells may comprise bacterial cells, yeast cells, as well as cultured (tissue) cell lines, inter alia, derived from mammals. Furthermore animals may also be employed as hosts, for example an non-human transgenic animal. Accordingly, said host (cell) may be transfected or transformed with the vector comprising a nucleic acid molecule coding for a polypeptide which is differentially regulated in pancreatic cancer as disclosed herein. Said host cell or host may therefore be genetically modified with a nucleic acid molecule encoding such a polypeptide or with a vector comprising such a nucleic acid molecule. The term "genetically modified" means that the host cell or host comprises in addition to its natural genome a nucleic acid molecule or vector coding for a polypeptide listed in tabels 2 and/or 3 or at least a fragment therof. Said additional genetic material may be introduced into the host (cell) or into one of its predecessors/parents. The nucleic acid molecule or vector may be present in the genetically modified host cell or host either as an independent molecule outside the genome, preferably as a molecule which is capable of replication, or it may be stably integrated into the genome of the host cell or host.

As mentioned herein above, the host cell of the present invention may be any prokaryotic or eukaryotic cell. Suitable prokaryotic cells are those generally used for cloning like E. coli or Bacillus subtilis. Yet, these prokaryotic host cells are also envisaged in the screening methods disclosed herein. Furthermore, eukaryotic cells comprise, for example, fungal or animal cells. Examples for suitable fungal cells are yeast cells, preferably those of the genus Saccharomyces and most preferably those of the species Saccharomyces cerevisiae. Suitable animal cells are, for instance, insect cells, vertebrate cells, preferably mammalian cells, such as e.g. CHO, HeLa, NIH3T3 or MOLT-4. Further suitable cell lines known in the art are obtainable from cell line depositories, like the American Type Culture Collection (ATCC).

The hosts may also be selected from non-human mammals, most preferably mice, rats, sheep, calves, dogs, monkeys or apes. As described herein above, said animals/mammals also comprise non-human transgenic animals, which preferably express at least one polypeptide differentially regulated in pancreatic cancer as disclosed herein. Preferably, said polypeptide is a polypeptide which is up-regulated in tissue derived from patients with pancreatic cancer. Yet it is also envisaged that non-human transgenic animals be produced which do not express marker genes as disclosed herein or who express limited amounts of said marker gene products. Said animals are preferably related to polypeptides which are down-regulated in pancreatic cancer. Transgenic non-human animals comprising and/or expressing the up-regulated polypeptides of the present invention or alternatively, which comprise silenced or less efficient versions of down-regulated polypeptides, are useful models for studying the development of pancreatic cancer and provide for useful models for testing drugs and therapeutics for pancreatic cancer treatment and/or prevention.

A compound which interacts with a polypeptide listed in tables 2 and/or 3 and which inhibits or antagonizes said polypeptide is identified by determining the activity of said polypeptide in the presence of said compound.

The term "activity" as used herein relates to the functional property or properties of a specific polypeptide. For the enzymes listed in tables 2 and/or 3, the term "activity" relates

to the enzymatic activity of a specific polypeptide. Activity assays for the enzymes listed in tables 2 and/or 3 are well known.

For adhesion molecules listed in tables 2 and/or 3, the term "activity" relates to the adhesive properties of a polypeptide and may determined using assays such as, but not limited to, adhesion assays, cell spreading assays, or in vitro interaction of the adhesion molecule with a known ligand. Such assays are well known in the art.

For cytoskeletal proteins, the term "activity" relates to the regulation of the cytoskeleton by such polypeptides, or to their incorporation into the cytoskeleton. As a non-limiting example, the ability of Gelsolin to regulate actin polymerization, or of Filamin A to promote orthogonal branching of actin filaments, may be determined using in vitro actin polymerization assays. Activity in relation to the regulation of cytoskeletal structures may further be determined by, as non-limiting examples, cell spreading assays, cell migration assays, cell proliferation assays or immunofluorecence assays, or by staining actin filaments with fluorescently labeled phalloidin. All of these assays are well known to the person skilled in the art.

For ion channels (Chloride intracellular channel protein) the term "activity" relates to ion flux (Chloride lux) across the membrane. Methods to determine ion flux across membranes are well known to the person skilled in the art.

For transcription factors, eg. KIAA 1034, the term "activity" relates to their ability to regulate gene transcription. The transcriptional activity of a polypeptide can be determined using commonly used assays, such as a reporter gene assay.

For growth factors and hormones or their receptors, the term "activity" relates to their ablitiy to bind to their receptors or ligands, respectively, and to induce receptor activation and subsequent signaling cascades, and/or it relates to the factor's or receptor's ability to mediate the cellular function or functions eventually caused by growth factor or

hormone mediated receptor activation. Growth factor or hormone binding to receptors can be determined by commonly known ligand binding assays. Receptor activation can be determined by testing for receptor autophosphorylation, or by assaying for modification or recruitment of downstream signaling mediators to the receptors (by immunoprecipitation and Western Blotting of signaling complexes). Cellular functions regulated by growth factors or hormones and their receptors can be cell proliferation (eg determined by using thymidine incorporation or cell counts), cell migration assays (eg determined by using modified Boyden chambers), cell survival or apoptosis assays (eg determined by using DAPI staining), angiogenesis assays (eg in vitro assays to measure endothelial tube formation that are commercially available). In addition to these assays, other assays may be used as well to determine these and other cellular functions.

Inhibitors or antagonists of a polypeptide listed in tables 2 and/or 3 are identified by the screening method described above when there is a decreased activity determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor or antagonist.

Further to the screening methods disclosed above, this invention provides a screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of a) contacting a host which expresses said polypeptide with a compound; b) determining the expression level and/or activity of said polypeptide; c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

An inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 is identified by the screening method described hereinbefore when a decreased expression of the protein is determined in the presence of the compound in comparison to the absence of the compound in the screening method, which is indicative for an inhibitor of expression of a polypeptide.

The term "express" as used herein relates to expression levels of a polypeptide listed in tables 2 and/or 3 which is up-regulated in pancreatic cancer, in cells, preferably in a pancreatic adenocarcinoma cell line, which are elevated as compared to the expression levels of the same polypeptide in healthy pancreatic cells. Preferably, expression levels are at least 2 fold, more preferably at least 3 fold, even more preferably at least 4 fold, most preferably at least 5 fold higher than in healthy pancreatic cells.

Furthermore, the present invention provides a compound identified and/or obtained by any of the screening methods hereinbefore described. Said compound is further comprised in a pharmaceutical composition. A method for the preparation of said pharmaceutical composition comprising formulating said compound in a pharmaceutically acceptable carrier or diluent is also claimed. Any conventional carrier material can be utilized. The carrier material can be an organic or inorganic one suitable for eteral, percutaneous or parenteral administration. Suitable carriers include water, gelatin, gum arabic, lactose, starch, magnesium stearate, talc, vegetable oils, polyalkylene-glycols, petroleum jelly and the like. Furthermore, the pharmaceutical preparations may contain other pharmaceutically active agents. Additional additives such as flavoring agents, stabilizers, emulsifying agents, buffers and the like may be added in accordance with accepted practices of pharmaceutical compounding.

Said compound may be used for the preparation of a medicament for the treatment or prevention of pancreatic cancer. In addition, said compound may also be used for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer. Preferably, said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

Within the scope of the present invention, antibodies against the proteins listed in table 2 and/or 3, or antigen-binding fragments thereof, may be used in an in vitro method for the diagnosis of pancreatic cancer.

In order to efficiently perform diagnostic screenings, the present invention provides a kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, described above. Another kit provided by this invention is a kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker hereinbefore described. Yet another kit provided by this invention is a kit for screening of compounds that antagonize any of the

polypeptides listed in tables 2 and/or 3, or inhibit the expression of any of said polypeptides.

In the present invention, the proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples are also claimed.

Examples:

Collection of tissue samples

Pancreatic carcinomas and adjacent tissue were collected from the patients listed in Table 1.

Samples were collected shortly after the resection (less than 30 minutes), and fast frozen in liquid nitrogen for about 1 minute, then stored in a freezer at a temperature of –80°C.

Characterization of formalin-fixed specimens

Histopathological characterization was carried out by using hematoxylin-eosin-stained sections of formalin-fixed and paraffin-embedded specimens. Tumors were classified using the WHO system. The types of pancreatic carcinomas included in the study are shown in Table 1.

The twelve pancreatic carcinoma samples used in this study were ductal carcinomas which constitute the overwhelming proportion of pancreatic carcinomas. The patient-matched samples from histologically normal tissue surrounding the carcinoma were used as controls. We carried out 12 pairs of 2-dimensional electrophoresis maps for comparing protein expression between tumor tissue and normal control tissue. For protein identification, the samples were pooled, thus generating pan-Carcinoma and pan-Normal protein extracts. Quantification was carried out in two steps: (I) Gels from the pooled samples were compared using the PDQuest image analysis software. (II) The changes identified at the level of the pooled samples were cross-validated by an analysis of the individual samples. The change factors shown in Tables 2 and 3 were determined using the pooled samples.

Preparation of samples for electrophoresis

Samples cleaned of clots and contaminating tissue were frozen in liquid nitrogen, then ground to powder. Samples were suspended in lysis buffer (8M urea, 4% CHAPS, 40mMol/L Tris-Cl, 0.5% carier amphollytes, 100mMol/L DTT and 0.1ìg/ìl PMSF) and centrifuged at 12000rpm for 30 minutes. The supernatants were stored at –80°C. The protein concentration in the extracts was determined by the Bradford method (Bradford, M. Anal. Biochem. 72, 248 (1976).

Two-dimensional gel electrophoresis

Samples containing 1 mg of protein were loaded onto the rehydrated IPG strip (18 cm, pH3~10) by using the cup loading method. IEF was performed using Pharmacia Multiphor apparatuses under the following conditions: First, the voltage was increased 200V-5000V over 24hrs, then a constant voltage of 5000V was applied for 24 hrs, the running temperature was 20°C. After IEF, the strips were equilibrated with 10 ml equilibration solution I (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 30 mM Dithioerythritol) for 15 min, then for another 15 min with equilibration solution II (6 M Urea, 50 mM Tris pH 8.8, 30 % Glycerol, 2.0 % SDS, 0.23 M Iodoacetamide).

The second dimension SDS polyacrylamide gel electrophoresis (SDS-PAGE) was carried out using a Hoefer ISO_DALT apparatus (10 gels/run, 24×20 cm), IEF strips were loaded onto 12% homogeneous polyacrylamide gels (1.5 mm x 24 cm × 20 cm). The gels were run in TGS_Buffer (250 mM Tris, 1.92 M Glycine, 1% (w/v) SDS, pH = 8.3, Bio-Rad) at a constant voltage (80 V, 20°C).

Gel fixation and staining

Gels were fixed in 50% Methanol/20% acetic acid for 30 min, then washed in ultra-pure water for 30 min and stained with NOVEX Colloidal Blue staining Kit (Invitrogen) following the manufacturer's recommendations.

Protein Identification

The protein identification was performed using a two-step procedure.

In-gel digestion

Spots were picked and transferred into 96-well by a spot picking robot. From each gel, 600-800 spots were picked. The spots were destained with 100µl of 30% acentonitrile in 50Mm ammonium bicarbonate, washed in ultra pure-water and dried in a speed vac evaporator. The dry gel pieces were digested with 10ng/µl trypsin (Promega, Madison, USA) solution in 500 nM ammonium bicarbonate at room temperature for 16 h maximum. The peptides from each spot were extracted with 20µl of 0.1% trifluore acetic acid (TFA) in 50% acetonitrile. The matrix solution consisted of 0.025%(w/v) alfa-cyano-4-hydroxy cinammic acid (Sigma) in 50% acetonitrile/0.1% TFA with internal standard peptides des-Arg-Bradykinin(Sigma, MW 904.4681 Da) and adrenocorticotropic hormone fragment 18-39 (Sigma, MW 2465.1989 Da).

Analysis by MALDI-TOF

1.5ul of peptide extract and 1.0µl of matrix solution were stimulaneously applied to the spots on the MS target. Recrytallization was carried out as specified by the instruments manufacturer. The samples were analyzed in a MALDI-time of flight Mass spectrometer (Autoflex, Bruker Analytics, Bremen, Germany). Peak annotation and database search by peptide matching was performed by in house developed software. The peptide mass was compared with theoretic peptide masses of all available proteins from all species. The monoisotopic mass was used and a mass tolerence of 0.0025% was allowed. 4 matching peptides were the minimal requirement for an identity assigment. Mismatch or miscleavage sites were not considered.

Table 1-Clinical and histopathological characteristics of samples

No. of Samples	Sex	Age	Tumor location	Histology	Metastasis in lymph nodes
PC-01	Male	48	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-02	Male	68	Head of pancreas	Poorly differentiated adenocarcinoma	Yes
PC-03	Male	44	Head of pancreas	Poorly differentiated ductal adenocarinoma, clear cell type	Yes
PC-04	Male	66	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-05	Female	45	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-06	Female	65	Head of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-07	Male	59	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-08	Female	62	Body of pancreas	Well differentiated ductal adenocarcinoma	Yes
PC-09	Male	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	No
PC-10	Female	53	Head of pancreas	Well differentiated ductal adenocarcinoma	No
PC-11	Female	54	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes
PC-12	Female	69	Head of pancreas	Middle differentiated ductal adenocarcinoma	Yes

Table 2: Proteins up-regulated in pancreatic cancer I

Protein	Acc No	Description	Seq ID No.	Fold Change
sw:CATD_HUMAN	P07339	Cathepsin D precursor (ec 3.4.23.5).	1	<2
sw:IDHC_HUMAN	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (ec 1.1.1.42)	2	2
sw:GELS_HUMAN	P06396	Gelsolin precursor, plasma	3	3
sw:CFAB_HUMAN	P00751	Complement factor B precursor (ec 3.4.21.47)	4	5
sw:AAC4_HUMAN	O43707	Alpha-actinin 4 (non-muscle alpha-actinin 4)	5	2
sw:AAC1_HUMAN	P12814	Alpha-actinin 1 (alpha-actinin cytoskeletal isoform)	7	2
sw:TBA4_HUMAN	P05215	Tubulin alpha-4 chain.	8	2
sw:ABP2_HUMAN	P21333	Filamin A (Endothelial actin-binding protein)	9	4
sw:TAGL_HUMAN	P37802	Transgelin 2 (smooth muscle protein 22-alpha)	10	2
sw:TPM4_HUMAN	P07226	Tropomyosin alpha 4 chain	11	<2
sw:BGH3_HUMAN	Q15582	Transforming growth factor-beta induced protein IG-H3 precursor	6	5
sw:CALD_HUMAN	Q05682	Caldesmon (cdm)	12	2
sw:ENOL_HUMAN	Q05524	Alpha enolase	13	2
sw:ACY1_HUMAN	Q03154	Aminoacylase-1	14	5
sw:CAPB_HUMAN	P47756	F-actin capping protein beta subunit (capz beta)	15	5
sw:IPYR_HUMAN	Q15181	Inorganic pyrophosphatase	16	<2
sw:LEG3_HUMAN	P17931	Galectin-3 (galactose-specific lectin 3).	17	2

sw:POR2_HUMAN	P45880	Voltage-dependent anion-selective channel protein 2	18	<2
SW:ANX2_HUMAN	P07355	Annexin II	19	2
sw:CBP2_HUMAN	P50454	Collagen-binding protein 2 precursor	20	2
sw:COF1_HUMAN	P23528	Cofilin, non-muscle isoform	21	<2
sw:CYPH_HUMAN	P05092	Peptidyl-prolyl cis-trans isomerase A	22	<2
sw:DYI2_HUMAN	Q13409	Dynein intermediate chain 2, cytosolic	23	2
sw:ECH1_HUMAN	Q13011	Delta3,5-Delta2,4-dienoyl-coa isomerase, mitochondrial precursor	24	2
sw:MLRN_HUMAN	P24844	Myosin regulatory light chain 2	48	2
sw:PLSL_HUMAN	P13796	L-Plastin	26	<2
sw:RAN_HUMAN	P17080	GTP-binding nuclear protein ran	27	3
sw:ROK_HUMAN	Q07244	Heterogeneous nuclear ribonucleoprotein k	28	2
sw:TCTP_HUMAN	P13693	Translationally controlled tumor	29	<2
sw:TPM1_HUMAN	P09493	Tropomyosin 1 alpha chain	30	<2
sw:TYPH_HUMAN	P19971	Thymidine phosphorylase precursor	31	5
sw:AMPL_HUMAN	P28838	Cytosol aminopeptidase	32	3
sw:K1CS_HUMAN	P08727	Keratin, type i cytoskeletal 19 (cytokeratin 19)	33	4
sw:ALDX_HUMAN	P14550	Alcohol dehydrogenase [NADP+]	34	4
sw:EL3A_HUMAN	P09093	Elastase IIIa precursor	35	4
sw:DLDH_HUMAN	P09622	Dihydrolipoamide dehydrogenase, mitochondrial precursor	36	2
sw:ECHM_HUMAN	P30084	Enoyl-CoA hydratase, mitochondrial precursor	37	3
sw:HSBX_HUMAN	O14558	Heat-shock 20 kDa like-protein p20.	38	2

sw:MLEN_HUMAN	P16475	Myosin light chain alkali, non-muscle isoform	39	3
sw:CALX_HUMAN	P27824	Calnexin precursor	40	3
sw:MA32_HUMAN	Q07021	Complement component 1	41	<2
sw:NUAM_HUMAN	P28331	NADH-ubiquinone oxidoreductase 75 kda subunit, mitochondrial precursor	42	2
sw:PBEF_HUMAN	P43490	Pre-B cell enhancing factor precursor.	43	2
sw:RET1_HUMAN	P09455	Retinol-binding protein I, cellular	44	2
sw:TCPG_HUMAN	P49368	T-complex protein 1, gamma subunit	45	2
sw:RINI_HUMAN	P13489	Placental ribonuclease inhibitor	46	<2
sw:GBLP_HUMAN	P25388	Guanine nucleotide-binding protein beta subunit-like protein 12.3	47	2
sw:S109_HUMAN	P06702	Calgranulin B	49	<2

Table 3: Proteins up-regulated in pancreatic cancer II

Protein	Acc No	Description	Seq ID No	Fold Change
sw:CAPG_HUMAN	P40121	Macrophage capping protein	50	3
sw:ANX1_HUMAN	P04083	Annexin I (lipocortin I) (calpactin II)	51	4
sw:K2C7_HUMAN	P08729	Keratin, type II cytoskeletal 7	52	5
humangp:CHR13-Q15063	Q15063	Osteoblast specific factor 2 precursor	53	2
sw:TGLC_HUMAN	P21980	Protein-glutamine gamma-glutamyltransferase	54	2
sw:GDIR_HUMAN	P52565	Rho GDP-dissociation inhibitor 1	55	<2
sw:IQG1_HUMAN	P46940	Ras GTPase-activating-like protein	25	2

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG

<120> Specific Markers for Pancreatic Cancer

<130> 5261 NDR

<160> 47

<170> PatentIn version 3.1

<210> 1

<211> 412

<212> PRT

<213> Homo sapiens

<220>

<221> Cathepsin D precursor

<222> (1)..(412)

<223> Swissprot accession No. as of 06 Dec 2002: P07339

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Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu Asp Leu Ile Ala
35 40 45

Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro Ala Val Thr Glu
50 55 60

Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp Ala Gln Tyr Tyr

65 70 75 80

Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe Thr Val Val Phe

85 90 95

Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Ile His Cys Lys Leu

100 105 110

Leu Asp Ile Ala Cys Trp Ile His His Lys Tyr Asn Ser Asp Lys Ser

115 120 125

Ser Thr Tyr Val Lys Asn Gly Thr Ser Phe Asp Ile His Tyr Gly Ser

130 135 140

Gly Ser Leu Ser Gly Tyr Leu Ser Gln Asp Thr Val Ser Val Pro Cys

145 150 155 160

Gln Ser Ala Ser Ser Ala Ser Ala Leu Gly Gly Val Lys Val Glu Arg

165 170 175

Gln Val Phe Gly Glu Ala Thr Lys Gln Pro Gly Ile Thr Phe Ile Ala

180 185 190

Ala Lys Phe Asp Gly Ile Leu Gly Met Ala Tyr Pro Arg Ile Ser Val

195 200 205

Asn Asn Val Leu Pro Val Phe Asp Asn Leu Met Gln Gln Lys Leu Val

210 215 220

Asp Gln Asn Ile Phe Ser Phe Tyr Leu Ser Arg Asp Pro Asp Ala Gln

225 230 235 240

Pro Gly Gly Glu Leu Met Leu Gly Gly Thr Asp Ser Lys Tyr Tyr Lys

245 250 255

Gly Ser Leu Ser Tyr Leu Asn Val Thr Arg Lys Ala Tyr Trp Gln Val

260 265 270

His Leu Asp Gln Val Glu Val Ala Ser Gly Leu Thr Leu Cys Lys Glu

275 280 285

Gly Cys Glu Ala Ile Val Asp Thr Gly Thr Ser Leu Met Val Gly Pro

290 295 300

Val Asp Glu Val Arg Glu Leu Gln Lys Ala Ile Gly Ala Val Pro Leu

305 310 315 320

Ile Gln Gly Glu Tyr Met Ile Pro Cys Glu Lys Val Ser Thr Leu Pro

325 330 335

Ala Ile Thr Leu Lys Leu Gly Gly Lys Gly Tyr Lys Leu Ser Pro Glu

340 345 350

Asp Tyr Thr Leu Lys Val Ser Gln Ala Gly Lys Thr Leu Cys Leu Ser

355 360 365

Gly Phe Met Gly Met Asp Ile Pro Pro Pro Ser Gly Pro Leu Trp Ile

370 375 380

Leu Gly Asp Val Phe Ile Gly Arg Tyr Tyr Thr Val Phe Asp Arg Asp

385 390 395 400

Asn Asn Arg Val Gly Phe Ala Glu Ala Ala Arg Leu

405 410

<210> 2

<211> 414

<212> PRT

<213> Homo sapiens

<220>

<221> Isocitrate dehydrogenase [NADP] cytoplasmic

<222> (1)..(414)

<223> Swissprot accession No. as of 06 Dec 2002: O75874

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20 25 30

Pro Tyr Val Glu Leu Asp Leu His Ser Tyr Asp Leu Gly Ile Glu Asn
35 40 45

Arg Asp Ala Thr Asn Asp Gln Val Thr Lys Asp Ala Ala Glu Ala Ile
50 55 60

Lys Lys His Asn Val Gly Val Lys Cys Ala Thr Ile Thr Pro Asp Glu
65 70 75 80

Lys Arg Val Glu Glu Phe Lys Leu Lys Gln Met Trp Lys Ser Pro Asn
85 90 95

Gly Thr Ile Arg Asn Ile Leu Gly Gly Thr Val Phe Arg Glu Ala Ile
100 105 110

Ile Cys Lys Asn Ile Pro Arg Leu Val Ser Gly Trp Val Lys Pro Ile
115 120 125

Ile Ile Gly Arg His Ala Tyr Gly Asp Gln Tyr Arg Ala Thr Asp Phe
130 135 140

Val Val Pro Gly Pro Gly Lys Val Glu Ile Thr Tyr Thr Pro Ser Asp
145 150 155 160

Gly Thr Gln Lys Val Thr Tyr Leu Val His Asn Phe Glu Glu Gly Gly
165 170 175

Gly Val Ala Met Gly Met Tyr Asn Gln Asp Lys Ser Ile Glu Asp Phe
180 185 190
Ala His Ser Ser Phe Gln Met Ala Leu Ser Lys Gly Trp Pro Leu Tyr
195 200 205
Leu Ser Thr Lys Asn Thr Ile Leu Lys Lys Tyr Asp Gly Arg Phe Lys
210 215 220
Asp Ile Phe Gln Glu Ile Tyr Asp Lys Gln Tyr Lys Ser Gln Phe Glu
225 230 235 240
Ala Gln Lys Ile Trp Tyr Glu His Arg Leu Ile Asp Asp Met Val Ala
245 250 255
Gln Ala Met Lys Ser Glu Gly Gly Phe Ile Trp Ala Cys Lys Asn Tyr
260 265 270
Asp Gly Asp Val Gln Ser Asp Ser Val Ala Gln Gly Tyr Gly Ser Leu
275 280 285
Gly Met Met Thr Ser Val Leu Val Cys Pro Asp Gly Lys Thr Val Glu
290 295 300
Ala Glu Ala Ala His Gly Thr Val Thr Arg His Tyr Arg Met Tyr Gln
305 310 315 320
Lys Gly Gln Glu Thr Ser Thr Asn Pro Ile Ala Ser Ile Phe Ala Trp
325 330 335
Thr Arg Gly Leu Ala His Arg Ala Lys Leu Asp Asn Asn Lys Glu Leu
340 345 350
Ala Phe Phe Ala Asn Ala Leu Glu Glu Val Ser Ile Glu Thr Ile Glu
355 360 365
Ala Gly Phe Met Thr Lys Asp Leu Ala Ala Cys Ile Lys Gly Leu Pro
370 375 380

Asn Val Gln Arg Ser Asp Tyr Leu Asn Thr Phe Glu Phe Met Asp Lys
385 390 395 400

Leu Gly Glu Asn Leu Lys Ile Lys Leu Ala Gln Ala Lys Leu
405 410

<210> 3

<211> 782

<212> PRT

<213> Homo sapiens

<220>

<221> Gelsolin precursor, plasma

<222> (1)..(782)

<223> swissprot accession No. as of 06 Dec 2002: P06396

<400> 3

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1 5 10 15

Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala Ala Thr Ala Ser Arg
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Gly Ala Ser Gln Ala Gly Ala Pro Gln Gly Arg Val Pro Glu Ala Arg
35 40 45

Pro Asn Ser Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys
50 55 60

Glu Pro Gly Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro

65 70 75 80

Val Pro Thr Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val

85 90 95

Ile Leu Lys Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu

100 105 110

His Tyr Trp Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala

115 120 125

Ala Ile Phe Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val

130 135 140

Gln His Arg Glu Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr

145 150 155 160

Phe Lys Ser Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe

165 170 175

Lys His Val Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val

180 185 190

Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu

195 200 205

Ser Phe Asn Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile

210 215 220

His Gln Trp Cys Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala

225 230 235 240

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala

245 250 255

Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln

260 265 270

Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala

275 280 285

Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser

290 295 300

Asn Gly Ala Gly Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro

305 310 315 320

Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His

325 330 335

Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr

340 345 350

Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys

355 360 365

Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly

370 375 380

Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp

385 390 395 400

Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn

405 410 415

Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala

420 425 430

Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln

435 440 445

Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr

450 455 460

Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr

465 470 475 480

Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala

485 490 495

Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln

500 505 510

Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln

515 520 525

Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met

530 535 540

Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro

545 550 555 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr

565 570 575

Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp

580 585 590

Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr

595 600 605

Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val

610 615 620

Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly

625 630 635 640

Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg

645 650 655

Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys

660 665 670

Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu

675 680 685

Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp

690 695 700

Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys

705 710 715 720

Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala

725 730 735

Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu

740 745 750

Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp

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Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala

770 775 780

<210> 4

<211> 764

<212> PRT

<213> Homo sapiens

<220>

<221> Complement factor B precursor

<222> (1)..(764)

<223> swissprot accession No. as of 06 Dec 2002: P00751

<400> 4

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35 40 45
Phe Arg Leu Leu Gln Glu Gly Gln Ala Leu Glu Tyr Val Cys Pro Ser
50 55 60
Gly Phe Tyr Pro Tyr Pro Val Gln Thr Arg Thr Cys Arg Ser Thr Gly
65 70 75 80
Ser Trp Ser Thr Leu Lys Thr Gln Asp Gln Lys Thr Val Arg Lys Ala
85 90 95
Glu Cys Arg Ala Ile His Cys Pro Arg Pro His Asp Phe Glu Asn Gly
100 105 110
Glu Tyr Trp Pro Arg Ser Pro Tyr Tyr Asn Val Ser Asp Glu Ile Ser
115 120 125
Phe His Cys Tyr Asp Gly Tyr Thr Leu Arg Gly Ser Ala Asn Arg Thr
130 135 140
Cys Gln Val Asn Gly Arg Trp Ser Gly Gln Thr Ala Ile Cys Asp Asn
145 150 155 160
Gly Ala Gly Tyr Cys Ser Asn Pro Gly Ile Pro Ile Gly Thr Arg Lys
165 170 175
Val Gly Ser Gln Tyr Arg Leu Glu Asp Ser Val Thr Tyr His Cys Ser
180 185 190
Arg Gly Leu Thr Leu Arg Gly Ser Gln Arg Arg Thr Cys Gln Glu Gly
195 200 205
Gly Ser Trp Ser Gly Thr Glu Pro Ser Cys Gln Asp Ser Phe Met Tyr
210 215 220

Asp Thr Pro Gln Glu Val Ala Glu Ala Phe Leu Ser Ser Leu Thr Glu
225 230 235 240
Thr Ile Glu Gly Val Asp Ala Glu Asp Gly His Gly Pro Gly Glu Gln
245 250 255
Gln Lys Arg Lys Ile Val Leu Asp Pro Ser Gly Ser Met Asn Ile Tyr
260 265 270
Leu Val Leu Asp Gly Ser Asp Ser Ile Gly Ala Ser Asn Phe Thr Gly
275 280 285
Ala Lys Lys Cys Leu Val Asn Leu Ile Glu Lys Val Ala Ser Tyr Gly
290 295 300
Val Lys Pro Arg Tyr Gly Leu Val Thr Tyr Ala Thr Tyr Pro Lys Ile
305 310 315 320
Trp Val Lys Val Ser Glu Ala Asp Ser Ser Asn Ala Asp Trp Val Thr
325 330 335
Lys Gln Leu Asn Glu Ile Asn Tyr Glu Asp His Lys Leu Lys Ser Gly
340 345 350
Thr Asn Thr Lys Lys Ala Leu Gln Ala Val Tyr Ser Met Met Ser Trp
355 360 365
Pro Asp Asp Val Pro Pro Glu Gly Trp Asn Arg Thr Arg His Val Ile
370 375 380
Ile Leu Met Thr Asp Gly Leu His Asn Met Gly Gly Asp Pro Ile Thr
385 390 395 400
Val Ile Asp Glu Ile Arg Asp Leu Leu Tyr Ile Gly Lys Asp Arg Lys
405 410 415
Asn Pro Arg Glu Asp Tyr Leu Asp Val Tyr Val Phe Gly Val Gly Pro
420 425 430

Leu Val Asn Gln Val Asn Ile Asn Ala Leu Ala Ser Lys Lys Asp Asn
435 440 445

Glu Gln His Val Phe Lys Val Lys Asp Met Glu Asn Leu Glu Asp Val
450 455 460

Phe Tyr Gln Met Ile Asp Glu Ser Gln Ser Leu Ser Leu Cys Gly Met
465 470 475 480

Val Trp Glu His Arg Lys Gly Thr Asp Tyr His Lys Gln Pro Trp Gln
485 490 495

Ala Lys Ile Ser Val Ile Arg Pro Ser Lys Gly His Glu Ser Cys Met
500 505 510

Gly Ala Val Val Ser Glu Tyr Phe Val Leu Thr Ala Ala His Cys Phe
515 520 525

Thr Val Asp Asp Lys Glu His Ser Ile Lys Val Ser Val Gly Gly Glu
530 535 540

Lys Arg Asp Leu Glu Ile Glu Val Val Leu Phe His Pro Asn Tyr Asn
545 550 555 560

Ile Asn Gly Lys Lys Glu Ala Gly Ile Pro Glu Phe Tyr Asp Tyr Asp
565 570 575

Val Ala Leu Ile Lys Leu Lys Asn Lys Leu Lys Tyr Gly Gln Thr Ile
580 585 590

Arg Pro Ile Cys Leu Pro Cys Thr Glu Gly Thr Thr Arg Ala Leu Arg
595 600 605

Leu Pro Pro Thr Thr Thr Cys Gln Gln Gln Lys Glu Glu Leu Leu Pro
610 615 620

Ala Gln Asp Ile Lys Ala Leu Phe Val Ser Glu Glu Glu Lys Lys Leu
625 630 635 640

Thr Arg Lys Glu Val Tyr Ile Lys Asn Gly Asp Lys Lys Gly Ser Cys
645 650 655

Glu Arg Asp Ala Gln Tyr Ala Pro Gly Tyr Asp Lys Val Lys Asp Ile
660 665 670

Ser Glu Val Val Thr Pro Arg Phe Leu Cys Thr Gly Gly Val Ser Pro
675 680 685

Tyr Ala Asp Pro Asn Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu Ile
690 695 700

Val His Lys Arg Ser Arg Phe Ile Gln Val Gly Val Ile Ser Trp Gly
705 710 715 720

Val Val Asp Val Cys Lys Asn Gln Lys Arg Gln Lys Gln Val Pro Ala
725 730 735

His Ala Arg Asp Phe His Ile Asn Leu Phe Gln Val Leu Pro Trp Leu
740 745 750

Lys Glu Lys Leu Gln Asp Glu Asp Leu Gly Phe Leu
755 760

<210> 5

<211> 911

<212> PRT

<213> Homo sapiens

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<221> Alpha-actinin 4

<222> (1)..(911)

<223> swissprot accession No. O43707

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Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp
35 40 45
Glu Lys Gln Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu
50 55 60
Arg Lys Ala Gly Thr Gln Ile Glu Asn Ile Asp Glu Asp Phe Arg Asp
65 70 75 80
Gly Leu Lys Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu
85 90 95
Pro Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val
100 105 110
Asn Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser
115 120 125
Ile Gly Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly
130 135 140
Met Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val
145 150 155 160
Glu Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys
165 170 175
Thr Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp

180 185 190

Lys Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu

195 200 205

Leu Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu

210 215 220

Asn Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met

225 230 235 240

Leu Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala

245 250 255

Ile Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln

260 265 270

Lys Ala Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn

275 280 285

Gln Glu Asn Glu His Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp

290 295 300

Leu Leu Glu Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asp Arg Val

305 310 315 320

Pro Gln Lys Thr Ile Gln Glu Met Gln Gln Lys Leu Glu Asp Phe Arg

325 330 335

Asp Tyr Arg Arg Val His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln

340 345 350

Leu Glu Ile Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn

355 360 365

Arg Pro Ala Phe Met Pro Ser Glu Gly Lys Met Val Ser Asp Ile Asn

370 375 380

Asn Gly Trp Gln His Leu Glu Gln Ala Glu Lys Gly Tyr Glu Glu Trp

385 390 395 400

Leu Leu Asn Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu

405 410 415

Lys Phe Arg Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys

420 425 430

Glu Ala Met Leu Lys His Arg Asp Tyr Glu Thr Ala Thr Leu Ser Asp

435 440 445

Ile Lys Ala Leu Ile Arg Lys His Glu Ala Phe Glu Ser Asp Leu Ala

450 455 460

Ala His Gln Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu

465 470 475 480

Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg Cys Gln

485 490 495

Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His Ser Arg

500 505 510

Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile Asp Gln

515 520 525

Leu His Leu Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met

530 535 540

Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val His Thr Ile

545 550 555 560

Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe Lys Ser Thr

565 570 575

Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu Ala Ile His Lys

580 585 590

Glu Ala Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser Gly Ser

595 600 605

Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys Trp Glu

610 615 620

Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu Glu Glu

625 630 635 640

Gln Ser Lys Gln Gln Ser Asn Glu His Leu Arg Arg Gln Phe Ala Ser

645 650 655

Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile

660 665 670

Gly Arg Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln Leu Ser

675 680 685

His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro Asn Leu

690 695 700

Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu Ile Phe

705 710 715 720

Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp

725 730 735

Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn

740 745 750

Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Gln

755 760 765

Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly Gly Ala

770 775 780

Leu Gly Pro Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp

785 790 795 800

Val Glu Asn Asp Arg Gln Gly Glu Ala Glu Phe Asn Arg Ile Met Ser

805 810 815

Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe Ile

820 825 830

Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln Val

835 840 845

Ile Ala Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr Ala

850 855 860

Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile

865 870 875 880

Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp Ala Val Pro Gly Ala Leu

885 890 895

Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

900 905 910

<210> 6

<211> 683

<212> PRT

<213> Homo sapiens

<220>

<221> Transforming growth factor-beta induced protein IG-H3 precursor

<222> (1)..(683)

<223> swissprot accession No. as of 06 Dec 2002: Q15582

<400> 6

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20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
210 215 220
Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
225 230 235 240
Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
245 250 255
Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
260 265 270
Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
275 280 285
Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
290 295 300
Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
305 310 315 320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
325 330 335
Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
340 345 350
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
355 360 365
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
370 375 380
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
385 390 395 400
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
405 410 415

Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg
420 425 430

Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr
435 440 445

Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg
450 455 460

Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala
465 470 475 480

Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg
485 490 495

Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp
500 505 510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
515 520 525

Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
530 535 540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
545 550 555 560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
565 570 575

Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
580 585 590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
595 600 605

Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
610 615 620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
625 630 635 640
Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
645 650 655
Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
660 665 670
Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
675 680

<210> 7
<211> 892
<212> PRT
<213> Homo sapiens
<220>
<221> Alpha-actinin 1
<222> (1)..(892)
<223> swissprot accession No. P12814

<400> 7

Met Asp His Tyr Asp Ser Gln Gln Thr Asn Asp Tyr Met Gln Pro Glu
1 5 10 15
Glu Asp Trp Asp Arg Asp Leu Leu Leu Asp Pro Ala Trp Glu Lys Gln
20 25 30
Gln Arg Lys Thr Phe Thr Ala Trp Cys Asn Ser His Leu Arg Lys Ala

35 40 45

Gly Thr Gln Ile Glu Asn Ile Glu Glu Asp Phe Arg Asp Gly Leu Lys

50 55 60

Leu Met Leu Leu Leu Glu Val Ile Ser Gly Glu Arg Leu Ala Lys Pro

65 70 75 80

Glu Arg Gly Lys Met Arg Val His Lys Ile Ser Asn Val Asn Lys Ala

85 90 95

Leu Asp Phe Ile Ala Ser Lys Gly Val Lys Leu Val Ser Ile Gly Ala

100 105 110

Glu Glu Ile Val Asp Gly Asn Val Lys Met Thr Leu Gly Met Ile Trp

115 120 125

Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu Glu Thr

130 135 140

Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr Ala Pro

145 150 155 160

Tyr Lys Asn Val Asn Ile Gln Asn Phe His Ile Ser Trp Lys Asp Gly

165 170 175

Leu Gly Phe Cys Ala Leu Ile His Arg His Arg Pro Glu Leu Ile Asp

180 185 190

Tyr Gly Lys Leu Arg Lys Asp Asp Pro Leu Thr Asn Leu Asn Thr Ala

195 200 205

Phe Asp Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu Asp Ala

210 215 220

Glu Asp Ile Val Gly Thr Ala Arg Pro Asp Glu Lys Ala Ile Met Thr

225 230 235 240

Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys Ala Glu

245 250 255

Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val Asn Gln Glu Asn

260 265 270

Glu Gln Leu Met Glu Asp Tyr Glu Lys Leu Ala Ser Asp Leu Leu Glu

275 280 285

Trp Ile Arg Arg Thr Ile Pro Trp Leu Glu Asn Arg Val Pro Glu Asn

290 295 300

Thr Met His Ala Met Gln Gln Lys Leu Glu Asp Phe Arg Asp Tyr Arg

305 310 315 320

Arg Leu His Lys Pro Pro Lys Val Gln Glu Lys Cys Gln Leu Glu Ile

325 330 335

Asn Phe Asn Thr Leu Gln Thr Lys Leu Arg Leu Ser Asn Arg Pro Ala

340 345 350

Phe Met Pro Ser Glu Gly Arg Met Val Ser Asp Ile Asn Asn Ala Trp

355 360 365

Gly Cys Leu Glu Gln Val Glu Lys Gly Tyr Glu Glu Trp Leu Leu Asn

370 375 380

Glu Ile Arg Arg Leu Glu Arg Leu Asp His Leu Ala Glu Lys Phe Arg

385 390 395 400

Gln Lys Ala Ser Ile His Glu Ala Trp Thr Asp Gly Lys Glu Ala Met

405 410 415

Leu Arg Gln Lys Asp Tyr Glu Thr Ala Thr Leu Ser Glu Ile Lys Ala

420 425 430

Leu Leu Lys Lys His Glu Ala Phe Glu Ser Asp Leu Ala Ala His Gln

435 440 445

Asp Arg Val Glu Gln Ile Ala Ala Ile Ala Gln Glu Leu Asn Glu Leu

450 455 460

Asp Tyr Tyr Asp Ser Pro Ser Val Asn Ala Arg Cys Gln Lys Ile Cys

465 470 475 480

Asp Gln Trp Asp Asn Leu Gly Ala Leu Thr Gln Lys Arg Arg Glu Ala

485 490 495

Leu Glu Arg Thr Glu Lys Leu Leu Glu Thr Ile Asp Gln Leu Tyr Leu

500 505 510

Glu Tyr Ala Lys Arg Ala Ala Pro Phe Asn Asn Trp Met Glu Gly Ala

515 520 525

Met Glu Asp Leu Gln Asp Thr Phe Ile Val His Thr Ile Glu Glu Ile

530 535 540

Gln Gly Leu Thr Thr Ala His Glu Gln Phe Lys Ala Thr Leu Pro Asp

545 550 555 560

Ala Asp Lys Glu Arg Leu Ala Ile Leu Gly Ile His Asn Glu Val Ser

565 570 575

Lys Ile Val Gln Thr Tyr His Val Asn Met Ala Gly Thr Asn Pro Tyr

580 585 590

Thr Thr Ile Thr Pro Gln Glu Ile Asn Gly Lys Trp Asp His Val Arg

595 600 605

Gln Leu Val Pro Arg Arg Asp Gln Ala Leu Thr Glu Glu His Ala Arg

610 615 620

Gln Gln His Asn Glu Ser Val Arg Lys Gln Phe Gly Ala Gln Ala Asn

625 630 635 640

Val Ile Gly Pro Trp Ile Gln Thr Lys Met Glu Glu Ile Gly Arg Ile

645 650 655

Ser Ile Glu Met His Gly Thr Leu Glu Asp Gln Leu Ser His Leu Arg

660 665 670

Gln Tyr Glu Lys Ser Ile Val Asn Tyr Lys Pro Lys Ile Asp Gln Leu

675 680 685

Glu Gly Asp His Gln Leu Ile Gln Glu Ala Leu Ile Phe Asp Asn Lys

690 695 700

His Thr Asn Tyr Thr Met Glu His Ile Arg Val Gly Trp Glu Gln Leu

705 710 715 720

Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val Glu Asn Gln Ile Leu

725 730 735

Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln Met Asn Glu Phe Arg

740 745 750

Ala Ser Phe Asn His Phe Asp Arg Asp His Ser Gly Thr Leu Gly Pro

755 760 765

Glu Glu Phe Lys Ala Cys Leu Ile Ser Leu Gly Tyr Asp Ile Gly Asn

770 775 780

Asp Pro Gln Gly Glu Ala Glu Phe Ala Arg Ile Met Ser Ile Val Asp

785 790 795 800

Pro Asn Arg Leu Gly Val Val Thr Phe Gln Ala Phe Ile Asp Phe Met

805 810 815

Ser Arg Glu Thr Ala Asp Thr Asp Thr Ala Asp Gln Val Met Ala Ser

820 825 830

Phe Lys Ile Leu Ala Gly Asp Lys Asn Tyr Ile Thr Met Asp Glu Leu

835 840 845

Arg Arg Glu Leu Pro Pro Asp Gln Ala Glu Tyr Cys Ile Ala Arg Met

850 855 860

Ala Pro Tyr Thr Gly Pro Asp Ser Val Pro Gly Ala Leu Asp Tyr Met

865 870 875 880

Ser Phe Ser Thr Ala Leu Tyr Gly Glu Ser Asp Leu

885 890

<210> 8

<211> 448

<212> PRT

<213> Homo sapiens

<220>

<221> Tubulin alpha-4 chain

<222> (1)..(448)

<223> swissprot accession No. P05215

<400> 8

Met Arg Glu Cys Ile Ser Val His Val Gly Gln Ala Gly Val Gln Met

1 5 10 15

Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile Gln Pro

20 25 30

Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp Asp Ser

35 40 45

Phe Thr Thr Phe Phe Cys Glu Thr Gly Ala Gly Lys His Val Pro Arg

50 55 60

Ala Val Phe Val Asp Leu Glu Pro Thr Val Ile Asp Glu Ile Arg Asn

65 70 75 80

Gly Pro Tyr Arg Gln Leu Phe His Pro Glu Gln Leu Ile Thr Gly Lys
85 90 95

Glu Asp Ala Ala Asn Asn Tyr Ala Arg Gly His Tyr Thr Ile Gly Lys
100 105 110

Glu Ile Ile Asp Pro Val Leu Asp Arg Ile Arg Lys Leu Ser Asp Gln
115 120 125

Cys Thr Gly Leu Gln Gly Phe Leu Val Phe His Ser Phe Gly Gly Gly
130 135 140

Thr Gly Ser Gly Phe Thr Ser Leu Leu Met Glu Arg Leu Ser Val Asp
145 150 155 160

Tyr Gly Lys Lys Ser Lys Leu Glu Phe Ser Ile Tyr Pro Ala Pro Gln
165 170 175

Val Ser Thr Ala Val Val Glu Pro Tyr Asn Ser Ile Leu Thr Thr His
180 185 190

Thr Thr Leu Glu His Ser Asp Cys Ala Phe Met Val Asp Asn Glu Ala
195 200 205

Ile Tyr Asp Ile Cys Arg Arg Asn Leu Asp Ile Glu Arg Pro Thr Tyr
210 215 220

Thr Asn Leu Asn Arg Leu Ile Ser Gln Ile Val Ser Ser Ile Thr Ala
225 230 235 240

Ser Leu Arg Phe Asp Gly Ala Leu Asn Val Asp Leu Thr Glu Phe Gln
245 250 255

Thr Asn Leu Val Pro Tyr Pro Arg Ile His Phe Pro Leu Ala Thr Tyr
260 265 270

Ala Pro Val Ile Ser Ala Glu Lys Ala Tyr His Glu Gln Leu Ser Val
275 280 285

Ala Glu Ile Thr Asn Ala Cys Phe Glu Pro Ala Asn Gln Met Val Lys
290 295 300

Cys Asp Pro Arg His Gly Lys Tyr Met Ala Cys Cys Leu Leu Tyr Arg
305 310 315 320

Gly Asp Val Val Pro Lys Asp Val Asn Ala Ala Ile Ala Ala Ile Lys
325 330 335

Thr Lys Arg Ser Ile Gln Phe Val Asp Trp Cys Pro Thr Gly Phe Lys
340 345 350

Val Gly Ile Asn Tyr Gln Pro Pro Thr Val Val Pro Gly Gly Asp Leu
355 360 365

Ala Lys Val Gln Arg Ala Val Cys Met Leu Ser Asn Thr Thr Ala Ile
370 375 380

Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met Tyr Ala
385 390 395 400

Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu Glu Gly
405 410 415

Glu Phe Ser Glu Ala Arg Glu Asp Met Ala Ala Leu Glu Lys Asp Tyr
420 425 430

Glu Glu Val Gly Ile Asp Ser Tyr Glu Asp Glu Asp Glu Gly Glu Glu
435 440 445

<210> 9

<211> 2647

<212> PRT

<213> Homo sapiens

<220>

<221> Filamin A

<222> (1)..(2647)

<223> swissprot accession No. P21333

<400> 9

Met Ser Ser Ser His Ser Arg Ala Gly Gln Ser Ala Ala Gly Ala Ala
1 5 10 15
Pro Gly Gly Gly Val Asp Thr Arg Asp Ala Glu Met Pro Ala Thr Glu
20 25 30
Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln Asn Thr
35 40 45
Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Ser Lys Arg Ile
50 55 60
Ala Asn Leu Gln Thr Asp Leu Ser Asp Gly Leu Arg Leu Ile Ala Leu
65 70 75 80
Leu Glu Val Leu Ser Gln Lys Lys Met His Arg Lys His Asn Gln Arg
85 90 95
Pro Thr Phe Arg Gln Met Gln Leu Glu Asn Val Ser Val Ala Leu Glu
100 105 110
Phe Leu Asp Arg Glu Ser Ile Lys Leu Val Ser Ile Asp Ser Lys Ala
115 120 125
Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp Thr Leu
130 135 140
Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Asp Glu Glu Glu Asp

145 150 155 160

Glu Glu Ala Lys Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly Trp Ile

165 170 175

Gln Asn Lys Leu Pro Gln Leu Pro Ile Thr Asn Phe Ser Arg Asp Trp

180 185 190

Gln Ser Gly Arg Ala Leu Gly Ala Leu Val Asp Ser Cys Ala Pro Gly

195 200 205

Leu Cys Pro Asp Trp Asp Ser Trp Asp Ala Ser Lys Pro Val Thr Asn

210 215 220

Ala Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Ile Pro Gln

225 230 235 240

Val Ile Thr Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu His Ser

245 250 255

Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys Pro Gly

260 265 270

Ala Pro Leu Arg Pro Lys Leu Asn Pro Lys Lys Ala Arg Ala Tyr Gly

275 280 285

Pro Gly Ile Glu Pro Thr Gly Asn Met Val Lys Lys Arg Ala Glu Phe

290 295 300

Thr Val Glu Thr Arg Ser Ala Gly Gln Gly Glu Val Leu Val Tyr Val

305 310 315 320

Glu Asp Pro Ala Gly His Gln Glu Glu Ala Lys Val Thr Ala Asn Asn

325 330 335

Asp Lys Asn Arg Thr Phe Ser Val Trp Tyr Val Pro Glu Val Thr Gly

340 345 350

Thr His Lys Val Thr Val Leu Phe Ala Gly Gln His Ile Ala Lys Ser

355 360 365

Pro Phe Glu Val Tyr Val Asp Lys Ser Gln Gly Asp Ala Ser Lys Val

370 375 380

Thr Ala Gln Gly Pro Gly Leu Glu Pro Ser Gly Asn Ile Ala Asn Lys

385 390 395 400

Thr Thr Tyr Phe Glu Ile Phe Thr Ala Gly Ala Gly Thr Gly Glu Val

405 410 415

Glu Val Val Ile Gln Asp Pro Met Gly Gln Lys Gly Thr Val Glu Pro

420 425 430

Gln Leu Glu Ala Arg Gly Asp Ser Thr Tyr Arg Cys Ser Tyr Gln Pro

435 440 445

Thr Met Glu Gly Val His Thr Val His Val Thr Phe Ala Gly Val Pro

450 455 460

Ile Pro Arg Ser Pro Tyr Thr Val Thr Val Gly Gln Ala Cys Asn Pro

465 470 475 480

Ser Ala Cys Arg Ala Val Gly Arg Gly Leu Gln Pro Lys Gly Val Arg

485 490 495

Val Lys Glu Thr Ala Asp Phe Lys Val Tyr Thr Lys Gly Ala Gly Ser

500 505 510

Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Glu Glu Arg Val

515 520 525

Lys Gln Lys Asp Leu Gly Asp Gly Val Tyr Gly Phe Glu Tyr Tyr Pro

530 535 540

Met Val Pro Gly Thr Tyr Ile Val Thr Ile Thr Trp Gly Gly Gln Asn

545 550 555 560

Ile Gly Arg Ser Pro Phe Glu Val Lys Val Gly Thr Glu Cys Gly Asn

565 570 575

Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Gly Gly Val Val Gly

580 585 590

Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Asp Asp Val Gly Thr

595 600 605

Leu Gly Phe Ser Val Glu Gly Pro Ser Gln Ala Lys Ile Glu Cys Asp

610 615 620

Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp Pro Gln Glu Ala

625 630 635 640

Gly Glu Tyr Ala Val His Val Leu Cys Asn Ser Glu Asp Ile Arg Leu

645 650 655

Ser Pro Phe Met Ala Asp Ile Arg Asp Ala Pro Gln Asp Phe His Pro

660 665 670

Asp Arg Val Lys Ala Arg Gly Pro Gly Leu Glu Lys Thr Gly Val Ala

675 680 685

Val Asn Lys Pro Ala Glu Phe Thr Val Asp Ala Lys His Gly Gly Lys

690 695 700

Ala Pro Leu Arg Val Gln Val Gln Asp Asn Glu Gly Cys Pro Val Glu

705 710 715 720

Ala Leu Val Lys Asp Asn Gly Asn Gly Thr Tyr Ser Cys Ser Tyr Val

725 730 735

Pro Arg Lys Pro Val Lys His Thr Ala Met Val Ser Trp Gly Gly Val

740 745 750

Ser Ile Pro Asn Ser Pro Phe Arg Val Asn Val Gly Ala Gly Ser His

755 760 765

Pro Asn Lys Val Lys Val Tyr Gly Pro Gly Val Ala Lys Thr Gly Leu

770 775 780

Lys Ala His Glu Pro Thr Tyr Phe Thr Val Asp Cys Ala Glu Ala Gly
785 790 795 800
Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro Gly Val Val Gly
805 810 815
Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Arg Asn Asp Asn Asp
820 825 830
Thr Phe Thr Val Lys Tyr Thr Pro Arg Gly Ala Gly Ser Tyr Thr Ile
835 840 845
Met Val Leu Phe Ala Asp Gln Ala Thr Pro Thr Ser Pro Ile Arg Val
850 855 860
Lys Val Glu Pro Ser His Asp Ala Ser Lys Val Lys Ala Glu Gly Pro
865 870 875 880
Gly Leu Ser Arg Thr Gly Val Glu Leu Gly Lys Pro Thr His Phe Thr
885 890 895
Val Asn Ala Lys Ala Ala Gly Lys Gly Lys Leu Asp Val Gln Phe Ser
900 905 910
Gly Leu Thr Lys Gly Asp Ala Val Arg Asp Val Asp Ile Ile Asp His
915 920 925
His Asp Asn Thr Tyr Thr Val Lys Tyr Thr Pro Val Gln Gln Gly Pro
930 935 940
Val Gly Val Asn Val Thr Tyr Gly Gly Asp Pro Ile Pro Lys Ser Pro
945 950 955 960
Phe Ser Val Ala Val Ser Pro Ser Leu Asp Leu Ser Lys Ile Lys Val
965 970 975
Ser Gly Leu Gly Glu Lys Val Asp Val Gly Lys Asp Gln Glu Phe Thr

980 985 990

Val Lys Ser Lys Gly Ala Gly Gly Gln Gly Lys Val Ala Ser Lys Ile

995 1000 1005

Val Gly Pro Ser Gly Ala Ala Val Pro Cys Lys Val Glu Pro Gly

1010 1015 1020

Leu Gly Ala Asp Asn Ser Val Val Arg Phe Leu Pro Arg Glu Glu

1025 1030 1035

Gly Pro Tyr Glu Val Glu Val Thr Tyr Asp Gly Val Pro Val Pro

1040 1045 1050

Gly Ser Pro Phe Pro Leu Glu Ala Val Ala Pro Thr Lys Pro Ser

1055 1060 1065

Lys Val Lys Ala Phe Gly Pro Gly Leu Gln Gly Gly Ser Ala Gly

1070 1075 1080

Ser Pro Ala Arg Phe Thr Ile Asp Thr Lys Gly Ala Gly Thr Gly

1085 1090 1095

Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Gln Leu Glu

1100 1105 1110

Cys Leu Asp Asn Gly Asp Gly Thr Cys Ser Val Ser Tyr Val Pro

1115 1120 1125

Thr Glu Pro Gly Asp Tyr Asn Ile Asn Ile Leu Phe Ala Asp Thr

1130 1135 1140

His Ile Pro Gly Ser Pro Phe Lys Ala His Val Val Pro Cys Phe

1145 1150 1155

Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu Glu Arg Ala

1160 1165 1170

Thr Ala Gly Glu Val Gly Gln Phe Gln Val Asp Cys Ser Ser Ala

1175 1180 1185

Gly Ser Ala Glu Leu Thr Ile Glu Ile Cys Ser Glu Ala Gly Leu

1190 1195 1200

Pro Ala Glu Val Tyr Ile Gln Asp His Gly Asp Gly Thr His Thr

1205 1210 1215

Ile Thr Tyr Ile Pro Leu Cys Pro Gly Ala Tyr Thr Val Thr Ile

1220 1225 1230

Lys Tyr Gly Gly Gln Pro Val Pro Asn Phe Pro Ser Lys Leu Gln

1235 1240 1245

Val Glu Pro Ala Val Asp Thr Ser Gly Val Gln Cys Tyr Gly Pro

1250 1255 1260

Gly Ile Glu Gly Gln Gly Val Phe Arg Glu Ala Thr Thr Glu Phe

1265 1270 1275

Ser Val Asp Ala Arg Ala Leu Thr Gln Thr Gly Gly Pro His Val

1280 1285 1290

Lys Ala Arg Val Ala Asn Pro Ser Gly Asn Leu Thr Glu Thr Tyr

1295 1300 1305

Val Gln Asp Arg Gly Asp Gly Met Tyr Lys Val Glu Tyr Thr Pro

1310 1315 1320

Tyr Glu Glu Gly Leu His Ser Val Asp Val Thr Tyr Asp Gly Ser

1325 1330 1335

Pro Val Pro Ser Ser Pro Phe Gln Val Pro Val Thr Glu Gly Cys

1340 1345 1350

Asp Pro Ser Arg Val Arg Val His Gly Pro Gly Ile Gln Ser Gly

1355 1360 1365

Thr Thr Asn Lys Pro Asn Lys Phe Thr Val Glu Thr Arg Gly Ala

1370 1375 1380

Gly Thr Gly Gly Leu Gly Leu Ala Val Glu Gly Pro Ser Glu Ala

1385 1390 1395

Lys Met Ser Cys Met Asp Asn Lys Asp Gly Ser Cys Ser Val Glu

1400 1405 1410

Tyr Ile Pro Tyr Glu Ala Gly Thr Tyr Ser Leu Asn Val Thr Tyr

1415 1420 1425

Gly Gly His Gln Val Pro Gly Ser Pro Phe Lys Val Pro Val His

1430 1435 1440

Asp Val Thr Asp Ala Ser Lys Val Lys Cys Ser Gly Pro Gly Leu

1445 1450 1455

Ser Pro Gly Met Val Arg Ala Asn Leu Pro Gln Ser Phe Gln Val

1460 1465 1470

Asp Thr Ser Lys Ala Gly Val Ala Pro Leu Gln Val Lys Val Gln

1475 1480 1485

Gly Pro Lys Gly Leu Val Glu Pro Val Asp Val Val Asp Asn Ala

1490 1495 1500

Asp Gly Thr Gln Thr Val Asn Tyr Val Pro Ser Arg Glu Gly Pro

1505 1510 1515

Tyr Ser Ile Ser Val Leu Tyr Gly Asp Glu Glu Val Pro Arg Ser

1520 1525 1530

Pro Phe Lys Val Lys Val Leu Pro Thr His Asp Ala Ser Lys Val

1535 1540 1545

Lys Ala Ser Gly Pro Gly Leu Asn Thr Thr Gly Val Pro Ala Ser

1550 1555 1560

Leu Pro Val Glu Phe Thr Ile Asp Ala Lys Asp Ala Gly Glu Gly

1565 1570 1575

Leu Leu Ala Val Gln Ile Thr Asp Pro Glu Gly Lys Pro Lys Lys

1580 1585 1590

Thr His Ile Gln Asp Asn His Asp Gly Thr Tyr Thr Val Ala Tyr

1595 1600 1605

Val Pro Asp Val Thr Gly Arg Tyr Thr Ile Leu Ile Lys Tyr Gly

1610 1615 1620

Gly Asp Glu Ile Pro Phe Ser Pro Tyr Arg Val Arg Ala Val Pro

1625 1630 1635

Thr Gly Asp Ala Ser Lys Cys Thr Val Thr Val Ser Ile Gly Gly

1640 1645 1650

His Gly Leu Gly Ala Gly Ile Gly Pro Thr Ile Gln Ile Gly Glu

1655 1660 1665

Glu Thr Val Ile Thr Val Asp Thr Lys Ala Ala Gly Lys Gly Lys

1670 1675 1680

Val Thr Cys Thr Val Cys Thr Pro Asp Gly Ser Glu Val Asp Val

1685 1690 1695

Asp Val Val Glu Asn Glu Asp Gly Thr Phe Asp Ile Phe Tyr Thr

1700 1705 1710

Ala Pro Gln Pro Gly Lys Tyr Val Ile Cys Val Arg Phe Gly Gly

1715 1720 1725

Glu His Val Pro Asn Ser Pro Phe Gln Val Thr Ala Leu Ala Gly

1730 1735 1740

Asp Gln Pro Ser Val Gln Pro Pro Leu Arg Ser Gln Gln Leu Ala

1745 1750 1755

Pro Gln Tyr Thr Tyr Ala Gln Gly Gly Gln Gln Thr Trp Ala Pro

1760 1765 1770

Glu Arg Pro Leu Val Gly Val Asn Gly Leu Asp Val Thr Ser Leu

1775 1780 1785

Arg Pro Phe Asp Leu Val Ile Pro Phe Thr Ile Lys Lys Gly Glu

1790 1795 1800

Ile Thr Gly Glu Val Arg Met Pro Ser Gly Lys Val Ala Gln Pro

1805 1810 1815

Thr Ile Thr Asp Asn Lys Asp Gly Thr Val Thr Val Arg Tyr Ala

1820 1825 1830

Pro Ser Glu Ala Gly Leu His Glu Met Asp Ile Arg Tyr Asp Asn

1835 1840 1845

Met His Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Tyr Val

1850 1855 1860

Asn Cys Gly His Val Thr Ala Tyr Gly Pro Gly Leu Thr His Gly

1865 1870 1875

Val Val Asn Lys Pro Ala Thr Phe Thr Val Asn Thr Lys Asp Ala

1880 1885 1890

Gly Glu Gly Gly Leu Ser Leu Ala Ile Glu Gly Pro Ser Lys Ala

1895 1900 1905

Glu Ile Ser Cys Thr Asp Asn Gln Asp Gly Thr Cys Ser Val Ser

1910 1915 1920

Tyr Leu Pro Val Leu Pro Gly Asp Tyr Ser Ile Leu Val Lys Tyr

1925 1930 1935

Asn Glu Gln His Val Pro Gly Ser Pro Phe Thr Ala Arg Val Thr

1940 1945 1950

Gly Asp Asp Ser Met Arg Met Ser His Leu Lys Val Gly Ser Ala

1955 1960 1965

Ala Asp Ile Pro Ile Asn Ile Ser Glu Thr Asp Leu Ser Leu Leu

1970 1975 1980

Thr Ala Thr Val Val Pro Pro Ser Gly Arg Glu Glu Pro Cys Leu

1985 1990 1995

Leu Lys Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro

2000 2005 2010

Lys Glu Thr Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln

2015 2020 2025

His Val Ala Ser Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu

2030 2035 2040

Ile Gly Asp Ala Ser Arg Val Arg Val Ser Gly Gln Gly Leu His

2045 2050 2055

Glu Gly His Thr Phe Glu Pro Ala Glu Phe Ile Ile Asp Thr Arg

2060 2065 2070

Asp Ala Gly Tyr Gly Gly Leu Ser Leu Ser Ile Glu Gly Pro Ser

2075 2080 2085

Lys Val Asp Ile Asn Thr Glu Asp Leu Glu Asp Gly Thr Cys Arg

2090 2095 2100

Val Thr Tyr Cys Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile

2105 2110 2115

Lys Phe Ala Asp Gln His Val Pro Gly Ser Pro Phe Ser Val Lys

2120 2125 2130

Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile Thr Arg Arg Arg

2135 2140 2145

Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys Asp Leu Ser

2150 2155 2160

Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala Gln Val

2165 2170 2175

Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu Gly

2180 2185 2190

Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly

2195 2200 2205

Thr His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly

2210 2215 2220

Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala

2225 2230 2235

His Lys Val Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala

2240 2245 2250

Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala

2255 2260 2265

Gly Gly Leu Ala Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile

2270 2275 2280

Ser Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ala Tyr Val

2285 2290 2295

Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Val Lys Phe Asn Glu

2300 2305 2310

Glu His Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Pro

2315 2320 2325

Ser Gly Asp Ala Arg Arg Leu Thr Val Ser Ser Leu Gln Glu Ser

2330 2335 2340

Gly Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Ser Leu Asn

2345 2350 2355

Gly Ala Lys Gly Ala Ile Asp Ala Lys Val His Ser Pro Ser Gly

2360 2365 2370

Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp Gln Asp Lys Tyr

2375 2380 2385

Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr Leu Ile Asp

2390 2395 2400

Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe Lys Ile

2405 2410 2415

Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val Ser

2420 2425 2430

Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala

2435 2440 2445

Glu Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser

2450 2455 2460

Val Thr Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu

2465 2470 2475

Cys Pro Glu Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly

2480 2485 2490

Ser Tyr Leu Ile Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly

2495 2500 2505

Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Val Ser

2510 2515 2520

Asn His Ser Leu His Glu Thr Ser Ser Val Phe Val Asp Ser Leu

2525 2530 2535

Thr Lys Ala Thr Cys Ala Pro Gln His Gly Ala Pro Gly Pro Gly

2540 2545 2550

Pro Ala Asp Ala Ser Lys Val Val Ala Lys Gly Leu Gly Leu Ser

2555 2560 2565

Lys Ala Tyr Val Gly Gln Lys Ser Ser Phe Thr Val Asp Cys Ser

2570 2575 2580

Lys Ala Gly Asn Asn Met Leu Leu Val Gly Val His Gly Pro Arg

2585 2590 2595

Thr Pro Cys Glu Glu Ile Leu Val Lys His Val Gly Ser Arg Leu

2600 2605 2610

Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly Glu Tyr Thr Leu

2615 2620 2625

Val Val Lys Trp Gly His Glu His Ile Pro Gly Ser Pro Tyr Arg

2630 2635 2640

Val Val Val Pro

2645

<210> 10

<211> 199

<212> PRT

<213> Homo sapiens

<220>

<221> Transgelin 2

<222> (1)..(199)

<223> swissprot accession No. as of 06 Dec 2002: P37802

<400> 10

Met Ala Asn Arg Gly Pro Ala Tyr Gly Leu Ser Arg Glu Val Gln Gln
1 5 10 15

Lys Ile Glu Lys Gln Tyr Asp Ala Asp Leu Glu Gln Ile Leu Ile Gln
20 25 30

Trp Ile Thr Thr Gln Cys Arg Lys Asp Val Gly Arg Pro Gln Pro Gly
35 40 45

Arg Glu Asn Phe Gln Asn Trp Leu Lys Asp Gly Thr Val Leu Cys Glu
50 55 60

Leu Ile Asn Ala Leu Tyr Pro Glu Gly Gln Ala Pro Val Lys Lys Ile
65 70 75 80

Gln Ala Ser Thr Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
85 90 95

Leu Gln Ala Ala Glu Arg Tyr Gly Ile Asn Thr Thr Asp Ile Phe Gln
100 105 110

Thr Val Asp Leu Trp Glu Gly Lys Asn Met Ala Cys Val Gln Arg Thr
115 120 125

Leu Met Asn Leu Gly Gly Leu Ala Val Ala Arg Asp Asp Gly Leu Phe
130 135 140

Ser Gly Asp Pro Asn Trp Phe Pro Lys Lys Ser Lys Glu Asn Pro Arg
145 150 155 160

Asn Phe Ser Asp Asn Gln Leu Gln Glu Gly Lys Asn Val Ile Gly Leu
165 170 175

Gln Met Gly Thr Asn Arg Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr
180 185 190

Gly Met Pro Arg Gln Ile Leu

195

<210> 11

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<221> Tropomyosin alpha 4 chain

<222> (1)..(248)

<223> swissprot accession No. P07226

<400> 11

Met Ala Gly Leu Asn Ser Leu Glu Ala Val Lys Arg Lys Ile Gln Ala

1 5 10 15

Leu Gln Gln Gln Ala Asp Glu Ala Glu Asp Arg Ala Gln Gly Leu Gln

20 25 30

Arg Glu Leu Asp Gly Glu Arg Glu Arg Arg Glu Lys Ala Glu Gly Asp

35 40 45

Val Ala Ala Leu Asn Arg Arg Ile Gln Leu Val Glu Glu Glu Leu Asp

50 55 60

Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala

65 70 75 80

Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn

85 90 95

Arg Ala Met Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu

100 105 110

Lys Glu Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu

115 120 125

Val Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu

130 135 140

Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu Glu

145 150 155 160

Leu Lys Asn Val Thr Asn Asn Leu Lys Ser Leu Glu Ala Ala Ser Glu

165 170 175

Lys Tyr Ser Glu Lys Glu Asp Lys Tyr Glu Glu Glu Ile Lys Leu Leu

180 185 190

Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe Ala Glu Arg

195 200 205

Thr Val Ala Lys Leu Glu Lys Thr Ile Asp Asp Leu Glu Glu Lys Leu

210 215 220

Ala Gln Ala Lys Glu Glu Asn Val Gly Leu His Gln Thr Leu Asp Gln

225 230 235 240

Thr Leu Asn Glu Leu Asn Cys Ile

245

<210> 12

<211> 793

<212> PRT

<213> Homo sapiens

<220>

<221> Caldesmon

<222> (1)..(793)

<223> swissprot accession No. as of 06 Dec 2002: Q05682

<400> 12

Met Asp Asp Phe Glu Arg Arg Arg Glu Leu Arg Arg Gln Lys Arg Glu
1 5 10 15

Glu Met Arg Leu Glu Ala Glu Arg Ile Ala Tyr Gln Arg Asn Asp Asp
20 25 30

Asp Glu Glu Glu Ala Ala Arg Glu Arg Arg Arg Arg Ala Arg Gln Glu
35 40 45

Arg Leu Arg Gln Lys Gln Glu Glu Glu Ser Leu Gly Gln Val Thr Asp
50 55 60

Gln Val Glu Val Asn Ala Gln Asn Ser Val Pro Asp Glu Glu Ala Lys
65 70 75 80

Thr Thr Thr Thr Asn Thr Gln Val Glu Gly Asp Asp Glu Ala Ala Phe
85 90 95

Leu Glu Arg Leu Ala Arg Arg Glu Glu Arg Arg Gln Lys Arg Leu Gln
100 105 110

Glu Ala Leu Glu Arg Gln Lys Glu Phe Asp Pro Thr Ile Thr Asp Ala
115 120 125

Ser Leu Ser Leu Pro Ser Arg Arg Met Gln Asn Asp Thr Ala Glu Asn
130 135 140

Glu Thr Thr Glu Lys Glu Glu Lys Ser Glu Ser Arg Gln Glu Arg Tyr

145 150 155 160

Glu Ile Glu Glu Thr Glu Thr Val Thr Lys Ser Tyr Gln Lys Asn Asp

165 170 175

Trp Arg Asp Ala Glu Glu Asn Lys Lys Glu Asp Lys Glu Lys Glu Glu

180 185 190

Glu Glu Glu Glu Lys Pro Lys Arg Gly Ser Ile Gly Glu Asn Gln Val

195 200 205

Glu Val Met Val Glu Glu Lys Thr Thr Glu Ser Gln Glu Glu Thr Val

210 215 220

Val Met Ser Leu Lys Asn Gly Gln Ile Ser Ser Glu Glu Pro Lys Gln

225 230 235 240

Glu Glu Glu Arg Glu Gln Gly Ser Asp Glu Ile Ser His His Glu Lys

245 250 255

Met Glu Glu Glu Asp Lys Glu Arg Ala Glu Ala Glu Arg Ala Arg Leu

260 265 270

Glu Ala Glu Glu Arg Glu Arg Ile Lys Ala Glu Gln Asp Lys Lys Ile

275 280 285

Ala Asp Glu Arg Ala Arg Ile Glu Ala Glu Glu Lys Ala Ala Ala Gln

290 295 300

Glu Arg Glu Arg Arg Glu Ala Glu Glu Arg Glu Arg Met Arg Glu Glu

305 310 315 320

Glu Lys Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys

325 330 335

Arg Ala Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala

340 345 350

Ala Glu Glu Arg Gln Arg Ile Lys Glu Glu Glu Lys Arg Ala Ala Glu

355 360 365

Glu Arg Gln Arg Ala Arg Ala Glu Glu Glu Glu Lys Ala Lys Val Glu

370 375 380

Glu Gln Lys Arg Asn Lys Gln Leu Glu Glu Lys Lys Arg Ala Met Gln

385 390 395 400

Glu Thr Lys Ile Lys Gly Glu Lys Val Glu Gln Lys Ile Glu Gly Lys

405 410 415

Trp Val Asn Glu Lys Lys Ala Gln Glu Asp Lys Leu Gln Thr Ala Val

420 425 430

Leu Lys Lys Gln Gly Glu Glu Lys Gly Thr Lys Val Gln Ala Lys Arg

435 440 445

Glu Lys Leu Gln Glu Asp Lys Pro Thr Phe Lys Lys Glu Glu Ile Lys

450 455 460

Asp Glu Lys Ile Lys Lys Asp Lys Glu Pro Lys Glu Glu Val Lys Ser

465 470 475 480

Phe Met Asp Arg Lys Lys Gly Phe Thr Glu Val Lys Ser Gln Asn Gly

485 490 495

Glu Phe Met Thr His Lys Leu Lys His Thr Glu Asn Thr Phe Ser Arg

500 505 510

Pro Gly Gly Arg Ala Ser Val Asp Thr Lys Glu Ala Glu Gly Ala Pro

515 520 525

Gln Val Glu Ala Gly Lys Arg Leu Glu Glu Leu Arg Arg Arg Arg Gly

530 535 540

Glu Thr Glu Ser Glu Glu Phe Glu Lys Leu Lys Gln Lys Gln Gln Glu

545 550 555 560

Ala Ala Leu Glu Leu Glu Glu Leu Lys Lys Lys Arg Glu Glu Arg Arg

565 570 575

Lys Val Leu Glu Glu Glu Glu Gln Arg Arg Lys Gln Glu Glu Ala Asp

580 585 590

Arg Lys Leu Arg Glu Glu Glu Glu Lys Arg Arg Leu Lys Glu Glu Ile

595 600 605

Glu Arg Arg Arg Ala Glu Ala Ala Glu Lys Arg Gln Lys Met Pro Glu

610 615 620

Asp Gly Leu Ser Asp Asp Lys Lys Pro Phe Lys Cys Phe Thr Pro Lys

625 630 635 640

Gly Ser Ser Leu Lys Ile Glu Glu Arg Ala Glu Phe Leu Asn Lys Ser

645 650 655

Val Gln Lys Ser Ser Gly Val Lys Ser Thr His Gln Ala Ala Ile Val

660 665 670

Ser Lys Ile Asp Ser Arg Leu Glu Gln Tyr Thr Ser Ala Ile Glu Gly

675 680 685

Thr Lys Ser Ala Lys Pro Thr Lys Pro Ala Ala Ser Asp Leu Pro Val

690 695 700

Pro Ala Glu Gly Val Arg Asn Ile Lys Ser Met Trp Glu Lys Gly Asn

705 710 715 720

Val Phe Ser Ser Pro Thr Ala Ala Gly Thr Pro Asn Lys Glu Thr Ala

725 730 735

Gly Leu Lys Val Gly Val Ser Ser Arg Ile Asn Glu Trp Leu Thr Lys

740 745 750

Thr Pro Asp Gly Asn Lys Ser Pro Ala Pro Lys Pro Ser Asp Leu Arg

755 760 765

Pro Gly Asp Val Ser Ser Lys Arg Asn Leu Trp Glu Lys Gln Ser Val

770 775 780

Asp Lys Val Thr Ser Pro Thr Lys Val

785 790

<210> 13

<211> 458

<212> PRT

<213> Homo sapiens

<220>

<221> Alpha enolase

<222> (1)..(458)

<223> swissprot accession No. as of 06 Dec 2002: Q05524

<400> 13

Met Ser Ile Leu Lys Ile Ile His Ala Arg Asp Ile Phe Glu Ser Arg

1 5 10 15

Gly Asn Pro Thr Val Glu Val Asp Leu Tyr Thr Asn Lys Gly Gly Leu

20 25 30

Phe Gly Arg Ala Ala Val Pro Ser Gly Ala Ser Thr Gly Ile Tyr Glu

35 40 45

Ala Leu Leu Glu Leu Arg Asp Asn Asp Lys Thr Arg Tyr Met Gly Gly

50 55 60

Lys Gly Val Ser Lys Ala Val Glu His Ile Ile Asn Lys Thr Ile Ala

65 70 75 80

Pro Ala Leu Ile Ser Lys Asn Val Asn Val Val Glu Gln Asp Lys Ile
85 90 95
Asp Asn Leu Met Leu Asp Met Asp Gly Ser Glu Asn Lys Ser Lys Phe
100 105 110
Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala Val Cys Ser Asn Ala
115 120 125
Gly Ala Thr Ala Glu Lys Gly Val Pro Leu Tyr Arg His Ile Ala Asp
130 135 140
Leu Ala Gly Asn Asn Pro Glu Val Ile Leu Pro Val Pro Ala Phe Asn
145 150 155 160
Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met Gln Glu
165 170 175
Phe Met Ile Pro Pro Cys Gly Ala Asp Arg Phe Asn Asp Ala Ile Arg
180 185 190
Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys Glu Lys
195 200 205
Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe Ala Pro
210 215 220
Asn Ile Leu Glu Asn Lys Glu Ala Leu Glu Leu Leu Lys Thr Ala Ile
225 230 235 240
Gly Lys Ala Gly Tyr Ser Asp Lys Val Val Ile Gly Met Asp Val Ala
245 250 255
Ala Ser Glu Phe Tyr Arg Asp Gly Lys Tyr Asp Leu Asp Phe Asn Ser
260 265 270
Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala Asp Leu
275 280 285

Tyr Lys Gly Phe Val Leu Gly His Ala Val Lys Asn Tyr Pro Val Gly
290 295 300

Val Ser Ile Glu Asp Pro Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp
305 310 315 320

Lys Lys Leu Phe Thr Gly Ser Leu Val Gly Ile Gln Val Val Gly Asp
325 330 335

Asp Leu Thr Val Thr Lys Pro Glu Ala Arg Ile Ala Lys Ala Val Glu
340 345 350

Glu Val Lys Ala Cys Asn Cys Leu Leu Leu Leu Lys Val Asn Gln Ile
355 360 365

Gly Ser Val Thr Glu Ser Leu Gln Ala Cys Lys Leu Ala Gln Ser Asn
370 375 380

Gly Trp Gly Val Met Pro Val Ser His Arg Leu Ser Gly Glu Thr Glu
385 390 395 400

Asp Thr Phe Met Ala Asp Leu Val Val Gly Leu Cys Thr Gly Gln Ile
405 410 415

Lys Thr Gly Pro Thr Cys Arg Ser Glu Arg Leu Ala Lys Tyr Asn Gln
420 425 430

Leu Leu Arg Ile Glu Glu Ala Glu Ala Gly Ser Lys Ala Arg Phe Ala
435 440 445

Gly Arg Asn Phe Arg Asn Pro Arg Ile Asn
450 455

<210> 14

<211> 408

<212> PRT

<213> Homo sapiens

<220>

<221> Aminoacylase-1

<222> (1)..(408)

<223> swissprot accession No. as of 06 Dec 2002: Q03154

<400> 14

Met Thr Ser Lys Gly Pro Glu Glu Glu His Pro Ser Val Thr Leu Phe
1 5 10 15

Arg Gln Tyr Leu Arg Ile Arg Thr Val Gln Pro Lys Pro Asp Tyr Gly
20 25 30

Ala Ala Val Ala Phe Phe Glu Glu Thr Ala Arg Gln Leu Gly Leu Gly
35 40 45

Cys Gln Lys Val Glu Val Ala Pro Gly Tyr Val Val Thr Val Leu Thr
50 55 60

Trp Pro Gly Thr Asn Pro Thr Leu Ser Ser Ile Leu Leu Asn Ser His
65 70 75 80

Thr Asp Val Val Pro Val Phe Lys Glu His Trp Ser His Asp Pro Phe
85 90 95

Glu Ala Phe Lys Asp Ser Glu Gly Tyr Ile Tyr Ala Arg Gly Ala Gln
100 105 110

Asp Met Lys Cys Val Ser Ile Gln Tyr Leu Glu Ala Val Arg Arg Leu
115 120 125

Lys Val Glu Gly His Arg Phe Pro Arg Thr Ile His Met Thr Phe Val

130 135 140

Pro Asp Glu Glu Val Gly Gly His Gln Gly Met Glu Leu Phe Val Gln

145 150 155 160

Arg Pro Glu Phe His Ala Leu Arg Ala Gly Phe Ala Leu Asp Glu Gly

165 170 175

Ile Ala Asn Pro Thr Asp Ala Phe Thr Val Phe Tyr Ser Glu Arg Ser

180 185 190

Pro Trp Trp Val Arg Val Thr Ser Thr Gly Arg Pro Gly His Ala Ser

195 200 205

Arg Phe Met Glu Asp Thr Ala Ala Glu Lys Leu His Lys Val Val Asn

210 215 220

Ser Ile Leu Ala Phe Arg Glu Lys Glu Trp Gln Arg Leu Gln Ser Asn

225 230 235 240

Pro His Leu Lys Glu Gly Ser Val Thr Ser Val Asn Leu Thr Lys Leu

245 250 255

Glu Gly Gly Val Ala Tyr Asn Val Ile Pro Ala Thr Met Ser Ala Ser

260 265 270

Phe Asp Phe Arg Val Ala Pro Asp Val Asp Phe Lys Ala Phe Glu Glu

275 280 285

Gln Leu Gln Ser Trp Cys Gln Ala Ala Gly Glu Gly Val Thr Leu Glu

290 295 300

Phe Ala Gln Lys Trp Met His Pro Gln Val Thr Pro Thr Asp Asp Ser

305 310 315 320

Asn Pro Trp Trp Ala Ala Phe Ser Arg Val Cys Lys Asp Met Asn Leu

325 330 335

Thr Leu Glu Pro Glu Ile Met Pro Ala Ala Thr Asp Asn Arg Tyr Ile

340 345 350

Arg Ala Val Gly Val Pro Ala Leu Gly Phe Ser Pro Met Asn Arg Thr

355 360 365

Pro Val Leu Leu His Asp His Asp Glu Arg Leu His Glu Ala Val Phe

370 375 380

Leu Arg Gly Val Asp Ile Tyr Thr Arg Leu Leu Pro Ala Leu Ala Ser

385 390 395 400

Val Pro Ala Leu Pro Ser Asp Ser

405

<210> 15

<211> 277

<212> PRT

<213> Homo sapiens

<220>

<221> F-actin capping protein beta subunit

<222> (1)..(277)

<223> swissprot accession No. as of 06 Dec 2002: P47756

<400> 15

Met Ser Asp Gln Gln Leu Asp Cys Ala Leu Asp Leu Met Arg Arg Leu

1 5 10 15

Pro Pro Gln Gln Ile Glu Lys Asn Leu Ser Asp Leu Ile Asp Leu Val

20 25 30

Pro Ser Leu Cys Glu Asp Leu Leu Ser Ser Val Asp Gln Pro Leu Lys
35 40 45

Ile Ala Arg Asp Lys Val Val Gly Lys Asp Tyr Leu Leu Cys Asp Tyr
50 55 60

Asn Arg Asp Gly Asp Ser Tyr Arg Ser Pro Trp Ser Asn Lys Tyr Asp
65 70 75 80

Pro Pro Leu Glu Asp Gly Ala Met Pro Ser Ala Arg Leu Arg Lys Leu
85 90 95

Glu Val Glu Ala Asn Asn Ala Phe Asp Gln Tyr Arg Asp Leu Tyr Phe
100 105 110

Glu Gly Gly Val Ser Ser Val Tyr Leu Trp Asp Leu Asp His Gly Phe
115 120 125

Ala Gly Val Ile Leu Ile Lys Lys Ala Gly Asp Gly Ser Lys Lys Ile
130 135 140

Lys Gly Cys Trp Asp Ser Ile His Val Val Glu Val Gln Glu Lys Ser
145 150 155 160

Ser Gly Arg Thr Ala His Tyr Lys Leu Thr Ser Thr Val Met Leu Trp
165 170 175

Leu Gln Thr Asn Lys Ser Gly Ser Gly Thr Met Asn Leu Gly Gly Ser
180 185 190

Leu Thr Arg Gln Met Glu Lys Asp Glu Thr Val Ser Asp Cys Ser Pro
195 200 205

His Ile Ala Asn Ile Gly Arg Leu Val Glu Asp Met Glu Asn Lys Ile
210 215 220

Arg Ser Thr Leu Asn Glu Ile Tyr Phe Gly Lys Thr Lys Asp Ile Val
225 230 235 240

Asn Gly Leu Arg Ser Ile Asp Ala Ile Pro Asp Asn Gln Lys Phe Lys
245 250 255

Gln Leu Gln Arg Glu Leu Ser Gln Val Leu Thr Gln Arg Gln Ile Tyr
260 265 270

Ile Gln Pro Asp Asn
275

<210> 16

<211> 289

<212> PRT

<213> Homo sapiens

<220>

<221> Inorganic pyrophosphatase

<222> (1)..(289)

<223> swissprot accession No. as of 06 Dec 2002: Q15181

<400> 16

Met Ser Gly Phe Ser Thr Glu Glu Arg Ala Ala Pro Phe Ser Leu Glu
1 5 10 15

Tyr Arg Val Phe Leu Lys Asn Glu Lys Gly Gln Tyr Ile Ser Pro Phe
20 25 30

His Asp Ile Pro Ile Tyr Ala Asp Lys Asp Val Phe His Met Val Val
35 40 45

Glu Val Pro Arg Trp Ser Asn Ala Lys Met Glu Ile Ala Thr Lys Asp

50 55 60

Pro Leu Asn Pro Ile Lys Gln Asp Val Lys Lys Gly Lys Leu Arg Tyr

65 70 75 80

Val Ala Asn Leu Phe Pro Tyr Lys Gly Tyr Ile Trp Asn Tyr Gly Ala

85 90 95

Ile Pro Gln Thr Trp Glu Asp Pro Gly His Asn Asp Lys His Thr Gly

100 105 110

Cys Cys Gly Asp Asn Asp Pro Ile Asp Val Cys Glu Ile Gly Ser Lys

115 120 125

Val Cys Ala Arg Gly Glu Ile Ile Gly Val Lys Val Leu Gly Ile Leu

130 135 140

Ala Met Ile Asp Glu Gly Glu Thr Asp Trp Lys Val Ile Ala Ile Asn

145 150 155 160

Val Asp Asp Pro Asp Ala Ala Asn Tyr Asn Asp Ile Asn Asp Val Lys

165 170 175

Arg Leu Lys Pro Gly Tyr Leu Glu Ala Thr Val Asp Trp Phe Arg Arg

180 185 190

Tyr Lys Val Pro Asp Gly Lys Pro Glu Asn Glu Phe Ala Phe Asn Ala

195 200 205

Glu Phe Lys Asp Lys Asp Phe Ala Ile Asp Ile Ile Lys Ser Thr His

210 215 220

Asp His Trp Lys Ala Leu Val Thr Lys Lys Thr Asn Gly Lys Gly Ile

225 230 235 240

Ser Cys Met Asn Thr Thr Leu Ser Glu Ser Pro Phe Lys Cys Asp Pro

245 250 255

Asp Ala Ala Arg Ala Ile Val Asp Ala Leu Pro Pro Pro Cys Glu Ser

260 265 270

Ala Cys Thr Val Pro Thr Asp Val Asp Lys Trp Phe His His Gln Lys

275 280 285

Asn

<210> 17

<211> 250

<212> PRT

<213> Homo sapiens

<220>

<221> Galectin-3 (Galactose-specific lectin 3)

<222> (1)..(250)

<223> swissprot accession No. as of 06 Dec 2002: P17931

<400> 17

Met Ala Asp Asn Phe Ser Leu His Asp Ala Leu Ser Gly Ser Gly Asn

1 5 10 15

Pro Asn Pro Gln Gly Trp Pro Gly Ala Trp Gly Asn Gln Pro Ala Gly

20 25 30

Ala Gly Gly Tyr Pro Gly Ala Ser Tyr Pro Gly Ala Tyr Pro Gly Gln

35 40 45

Ala Pro Pro Gly Ala Tyr Pro Gly Gln Ala Pro Pro Gly Ala Tyr His

50 55 60

Gly Ala Pro Gly Ala Tyr Pro Gly Ala Pro Ala Pro Gly Val Tyr Pro

65 70 75 80

Gly Pro Pro Ser Gly Pro Gly Ala Tyr Pro Ser Ser Gly Gln Pro Ser

85 90 95

Ala Pro Gly Ala Tyr Pro Ala Thr Gly Pro Tyr Gly Ala Pro Ala Gly

100 105 110

Pro Leu Ile Val Pro Tyr Asn Leu Pro Leu Pro Gly Gly Val Val Pro

115 120 125

Arg Met Leu Ile Thr Ile Leu Gly Thr Val Lys Pro Asn Ala Asn Arg

130 135 140

Ile Ala Leu Asp Phe Gln Arg Gly Asn Asp Val Ala Phe His Phe Asn

145 150 155 160

Pro Arg Phe Asn Glu Asn Asn Arg Arg Val Ile Val Cys Asn Thr Lys

165 170 175

Leu Asp Asn Asn Trp Gly Arg Glu Glu Arg Gln Ser Val Phe Pro Phe

180 185 190

Glu Ser Gly Lys Pro Phe Lys Ile Gln Val Leu Val Glu Pro Asp His

195 200 205

Phe Lys Val Ala Val Asn Asp Ala His Leu Leu Gln Tyr Asn His Arg

210 215 220

Val Lys Lys Leu Asn Glu Ile Ser Lys Leu Gly Ile Ser Gly Asp Ile

225 230 235 240

Asp Leu Thr Ser Ala Ser Tyr Thr Met Ile

245 250

<210> 18

<211> 347

<212> PRT

<213> Homo sapiens

<220>

<221> Voltage-dependent anion-selective channel protein 2 (VDAC-2)

<222> (1)..(347)

<223> swissprot accession No.as of 06 Dec 2002: P45880

<400> 18

Met Ser Trp Cys Asn Glu Leu Arg Leu Pro Ala Leu Lys Gln His Ser
1 5 10 15
Ile Gly Arg Gly Leu Glu Ser His Ile Thr Met Cys Ile Pro Pro Ser
20 25 30
Tyr Ala Asp Leu Gly Lys Ala Ala Arg Asp Ile Phe Asn Lys Gly Phe
35 40 45
Gly Phe Gly Leu Val Lys Leu Asp Val Lys Thr Lys Ser Cys Ser Gly
50 55 60
Val Glu Phe Ser Thr Ser Gly Ser Ser Asn Thr Asp Thr Gly Lys Val
65 70 75 80
Thr Gly Thr Leu Glu Thr Lys Tyr Lys Trp Cys Glu Tyr Gly Leu Thr
85 90 95
Phe Thr Glu Lys Trp Asn Thr Asp Asn Thr Leu Gly Thr Glu Ile Ala
100 105 110
Ile Glu Asp Gln Ile Cys Gln Gly Leu Lys Leu Thr Phe Asp Thr Thr

115 120 125

Phe Ser Pro Asn Thr Gly Lys Lys Ser Gly Lys Ile Lys Ser Ser Tyr

130 135 140

Lys Arg Glu Cys Ile Asn Leu Gly Cys Asp Val Asp Phe Asp Phe Ala

145 150 155 160

Gly Pro Ala Ile His Gly Ser Ala Val Phe Gly Tyr Glu Gly Trp Leu

165 170 175

Ala Gly Tyr Gln Met Thr Phe Asp Ser Ala Lys Ser Lys Leu Thr Arg

180 185 190

Asn Asn Phe Ala Val Gly Tyr Arg Thr Gly Asp Phe Gln Leu His Thr

195 200 205

Asn Val Asn Asp Gly Thr Glu Phe Gly Gly Ser Ile Tyr Gln Lys Val

210 215 220

Cys Glu Asp Leu Asp Thr Ser Val Asn Leu Ala Trp Thr Ser Gly Thr

225 230 235 240

Asn Cys Thr Arg Phe Gly Ile Ala Ala Lys Tyr Gln Leu Asp Pro Thr

245 250 255

Ala Ser Ile Ser Ala Lys Val Asn Asn Ser Ser Leu Ile Gly Val Gly

260 265 270

Tyr Thr Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu

275 280 285

Val Asp Gly Lys Ser Ile Asn Ala Gly Gly His Lys Val Gly Ser Pro

290 295 300

Trp Ser Trp Arg Leu Asn Pro Ala Glu Arg Asn Leu Trp Glu Trp Ile

305 310 315 320

Ser Glu Asp Leu Ala Leu Ile Tyr Phe His Cys Asp Gln Gln Gln Ala

325 330 335

Phe Phe Pro Pro Glu Asp Asp Gln Asn Lys Gly

340 345

<210> 19

<211> 339

<212> PRT

<213> Homo sapiens

<220>

<221> Annexin II

<222> (1)..(339)

<223> swissprot accession No. as of 06 Dec 2002: P07355

<400> 19

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp

1 5 10 15

His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn

20 25 30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr

35 40 45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser

50 55 60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys

65 70 75 80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu
85 90 95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser
100 105 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
115 120 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
130 135 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
145 150 155 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
165 170 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
180 185 190

Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
195 200 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
210 215 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
225 230 235 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
245 250 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
260 265 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
275 280 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
290 295 300
Ser Glu Phe Lys Arg Lys Tyr Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
305 310 315 320
Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly
325 330 335
Gly Asp Asp

<210> 20
<211> 418
<212> PRT
<213> Homo sapiens
<220>
<221> Collagen-binding protein 2 precursor
<222> (1)..(418)
<223> swissprot accession No. P50454
<400> 20

Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
1 5 10 15
Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
20 25 30
Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
35 40 45

Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
50 55 60
Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
65 70 75 80
Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
85 90 95
Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
100 105 110
Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
115 120 125
Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
130 135 140
Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
145 150 155 160
Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
165 170 175
Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
180 185 190
Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
195 200 205
His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
210 215 220
Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
225 230 235 240
Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
245 250 255

Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
260 265 270
His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
275 280 285
Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
290 295 300
Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
305 310 315 320
Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
325 330 335
Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
340 345 350
His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
355 360 365
Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
370 375 380
Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu
385 390 395 400
Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp
405 410 415
Glu Leu

<210> 21

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> Cofilin, non-muscle isoform

<222> (1)..(166)

<223> swissprot accession No. as of 08 ec 2002: P23528

<400> 21

Met Ala Ser Gly Val Ala Val Ser Asp Gly Val Ile Lys Val Phe Asn
1 5 10 15

Asp Met Lys Val Arg Lys Ser Ser Thr Pro Glu Glu Val Lys Lys Arg
20 25 30

Lys Lys Ala Val Leu Phe Cys Leu Ser Glu Asp Lys Lys Asn Ile Ile
35 40 45

Leu Glu Glu Gly Lys Glu Ile Leu Val Gly Asp Val Gly Gln Thr Val
50 55 60

Asp Asp Pro Tyr Ala Thr Phe Val Lys Met Leu Pro Asp Lys Asp Cys
65 70 75 80

Arg Tyr Ala Leu Tyr Asp Ala Thr Tyr Glu Thr Lys Glu Ser Lys Lys
85 90 95

Glu Asp Leu Val Phe Ile Phe Trp Ala Pro Glu Ser Ala Pro Leu Lys
100 105 110

Ser Lys Met Ile Tyr Ala Ser Ser Lys Asp Ala Ile Lys Lys Lys Leu
115 120 125

Thr Gly Ile Lys His Glu Leu Gln Ala Asn Cys Tyr Glu Glu Val Lys

130 135 140

Asp Arg Cys Thr Leu Ala Glu Lys Leu Gly Gly Ser Ala Val Ile Ser

145 150 155 160

Leu Glu Gly Lys Pro Leu

165

<210> 22

<211> 165

<212> PRT

<213> Homo sapiens

<220>

<221> Peptidyl-prolyl cis-trans isomerase A

<222> (1)..(165)

<223> swissprot accession No. as of 09 ec 2002: P05092

<400> 22

Met Val Asn Pro Thr Val Phe Phe Asp Ile Ala Val Asp Gly Glu Pro

1 5 10 15

Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr

20 25 30

Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr

35 40 45

Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly

50 55 60

Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly
65 70 75 80
Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly
85 90 95
Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe
100 105 110
Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val
115 120 125
Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg
130 135 140
Phe Gly Ser Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ile Ala Asp
145 150 155 160
Cys Gly Gln Leu Glu
165

<210> 23
<211> 638
<212> PRT
<213> Homo sapiens
<220>
<221> Dynein intermediate chain 2, cytosolic
<222> (1)..(638)
<223> swisprot accession No. as of 09 Dec 2002: Q13409

<400> 23

Met Ser Asp Lys Ser Glu Leu Lys Ala Glu Leu Glu Arg Lys Lys Gln
1 5 10 15
Arg Leu Ala Gln Ile Arg Glu Glu Lys Lys Arg Lys Glu Glu Glu Arg
20 25 30
Lys Lys Lys Glu Thr Asp Gln Lys Lys Glu Ala Val Ala Pro Val Gln
35 40 45
Glu Glu Ser Asp Leu Glu Lys Lys Arg Arg Glu Ala Glu Ala Leu Leu
50 55 60
Gln Ser Met Gly Leu Thr Pro Glu Ser Pro Ile Val Phe Ser Glu Tyr
65 70 75 80
Trp Val Pro Pro Pro Met Ser Pro Ser Ser Lys Ser Val Ser Thr Pro
85 90 95
Ser Glu Ala Gly Ser Gln Asp Ser Gly Asp Gly Ala Val Gly Ser Arg
100 105 110
Thr Leu His Trp Asp Thr Asp Pro Ser Val Leu Gln Leu His Ser Asp
115 120 125
Ser Asp Leu Gly Arg Gly Pro Ile Lys Leu Gly Met Ala Lys Ile Thr
130 135 140
Gln Val Asp Phe Pro Pro Arg Glu Ile Val Thr Tyr Thr Lys Glu Thr
145 150 155 160
Gln Thr Pro Val Met Ala Gln Pro Lys Glu Asp Glu Glu Glu Asp Asp
165 170 175
Asp Val Val Ala Pro Lys Pro Pro Ile Glu Pro Glu Glu Glu Lys Thr
180 185 190
Leu Lys Lys Asp Glu Glu Asn Asp Ser Lys Ala Pro Pro His Glu Leu

195 200 205

Thr Glu Glu Glu Lys Gln Gln Ile Leu His Ser Glu Glu Phe Leu Ser

210 215 220

Phe Phe Asp His Ser Thr Arg Ile Val Glu Arg Ala Leu Ser Glu Gln

225 230 235 240

Ile Asn Ile Phe Phe Asp Tyr Ser Gly Arg Asp Leu Glu Asp Lys Glu

245 250 255

Gly Glu Ile Gln Ala Gly Ala Lys Leu Ser Leu Asn Arg Gln Phe Phe

260 265 270

Asp Glu Arg Trp Ser Lys His Arg Val Val Ser Cys Leu Asp Trp Ser

275 280 285

Ser Gln Tyr Pro Glu Leu Leu Val Ala Ser Tyr Asn Asn Asn Glu Asp

290 295 300

Ala Pro His Glu Pro Asp Gly Val Ala Leu Val Trp Asn Met Lys Tyr

305 310 315 320

Lys Lys Thr Thr Pro Glu Tyr Val Phe His Cys Gln Ser Ala Val Met

325 330 335

Ser Ala Thr Phe Ala Lys Phe His Pro Asn Leu Val Val Gly Gly Thr

340 345 350

Tyr Ser Gly Gln Ile Val Leu Trp Asp Asn Arg Ser Asn Lys Arg Thr

355 360 365

Pro Val Gln Arg Thr Pro Leu Ser Ala Ala Ala His Thr His Pro Val

370 375 380

Tyr Cys Val Asn Val Val Gly Thr Gln Asn Ala His Asn Leu Ile Ser

385 390 395 400

Ile Ser Thr Asp Gly Lys Ile Cys Ser Trp Ser Leu Asp Met Leu Ser

405 410 415

His Pro Gln Asp Ser Met Glu Leu Val His Lys Gln Ser Lys Ala Val

420 425 430

Ala Val Thr Ser Met Ser Phe Pro Val Gly Asp Val Asn Asn Phe Val

435 440 445

Val Gly Ser Glu Glu Gly Ser Val Tyr Thr Ala Cys Arg His Gly Ser

450 455 460

Lys Ala Gly Ile Ser Glu Met Phe Glu Gly His Gln Gly Pro Ile Thr

465 470 475 480

Gly Ile His Cys His Ala Ala Val Gly Ala Val Asp Phe Ser His Leu

485 490 495

Phe Val Thr Ser Ser Phe Asp Trp Thr Val Lys Leu Trp Thr Thr Lys

500 505 510

Asn Asn Lys Pro Leu Tyr Ser Phe Glu Asp Asn Ala Asp Tyr Val Tyr

515 520 525

Asp Val Met Trp Ser Pro Thr His Pro Ala Leu Phe Ala Cys Val Asp

530 535 540

Gly Met Gly Arg Leu Asp Leu Trp Asn Leu Asn Asn Asp Thr Glu Val

545 550 555 560

Pro Thr Ala Ser Ile Ser Val Glu Gly Asn Pro Ala Leu Asn Arg Val

565 570 575

Arg Trp Thr His Ser Gly Arg Glu Ile Ala Val Gly Asp Ser Glu Gly

580 585 590

Gln Ile Val Ile Tyr Asp Val Gly Glu Gln Ile Ala Val Pro Arg Asn

595 600 605

Asp Glu Trp Ala Arg Phe Gly Arg Thr Leu Ala Glu Ile Asn Ala Asn

610 615 620

Arg Ala Asp Ala Glu Glu Glu Ala Ala Thr Arg Ile Pro Ala

625 630 635

<210> 24

<211> 328

<212> PRT

<213> Homo sapiens

<220>

<221> Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor

<222> (1)..(328)

<223> swissprot accession No. as of 09 Dec 2002: Q13011

<400> 24

Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr

1 5 10 15

Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg

20 25 30

Leu Thr Gly Ser Ser Ala Gln Glu Glu Ala Ser Gly Val Ala Leu Gly

35 40 45

Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln

50 55 60

Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala

65 70 75 80

Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile
85 90 95
Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys
100 105 110
Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu
115 120 125
Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp
130 135 140
Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro
145 150 155 160
Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Gly Val
165 170 175
Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe
180 185 190
Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr
195 200 205
Leu Glu Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val Asn Glu
210 215 220
Leu Ala Phe Thr Ala His Lys Met Met Ala Asp Glu Ala Leu Asp Ser
225 230 235 240
Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala
245 250 255
Ala Leu Pro Leu Ala Pro Glu Ile Ser Ser Lys Thr Thr Val Leu Val
260 265 270
Gln Ser Thr Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala
275 280 285

Glu Ser Leu Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr
290 295 300

Gln Asp Leu Val Lys Ser Val Gln Pro Thr Thr Glu Asn Lys Glu Leu
305 310 315 320

Lys Thr Val Thr Phe Ser Lys Leu
325

<210> 25
<211> 1657
<212> PRT
<213> Homo sapiens
<220>
<221> Ras GTPase-activating-like protein IQGAP1
<222> (1)..(1657)
<223> swissprot accession No. as of 09 Dec 2002: P46940

<400> 25

Met Ser Ala Ala Asp Glu Val Asp Gly Leu Gly Val Ala Arg Pro His
1 5 10 15

Tyr Gly Ser Val Leu Asp Asn Glu Arg Leu Thr Ala Glu Glu Met Asp
20 25 30

Glu Arg Arg Arg Gln Asn Val Ala Tyr Glu Tyr Leu Cys His Leu Glu
35 40 45

Glu Ala Lys Arg Trp Met Glu Ala Cys Leu Gly Glu Asp Leu Pro Pro

50 55 60

Thr Thr Glu Leu Glu Glu Gly Leu Arg Asn Gly Val Tyr Leu Ala Lys
65 70 75 80

Leu Gly Asn Phe Phe Ser Pro Lys Val Val Ser Leu Lys Lys Ile Tyr
85 90 95

Asp Arg Glu Gln Thr Arg Tyr Lys Ala Thr Gly Leu His Phe Arg His
100 105 110

Thr Asp Asn Val Ile Gln Trp Leu Asn Ala Met Asp Glu Ile Gly Leu
115 120 125

Pro Lys Ile Phe Tyr Pro Glu Thr Thr Asp Ile Tyr Asp Arg Lys Asn
130 135 140

Met Pro Arg Cys Ile Tyr Cys Ile His Ala Leu Ser Leu Tyr Leu Phe
145 150 155 160

Lys Leu Gly Leu Ala Pro Gln Ile Gln Asp Leu Tyr Gly Lys Val Asp
165 170 175

Phe Thr Glu Glu Glu Ile Asn Asn Met Lys Thr Glu Leu Glu Lys Tyr
180 185 190

Gly Ile Gln Met Pro Ala Phe Ser Lys Ile Gly Gly Ile Leu Ala Asn
195 200 205

Glu Leu Ser Val Asp Glu Ala Ala Leu His Ala Ala Val Ile Ala Ile
210 215 220

Asn Glu Ala Ile Asp Arg Arg Ile Pro Ala Asp Thr Phe Ala Ala Leu
225 230 235 240

Lys Asn Pro Asn Ala Met Leu Val Asn Leu Glu Glu Pro Leu Ala Ser
245 250 255

Thr Tyr Gln Asp Ile Leu Tyr Gln Ala Lys Gln Asp Lys Met Thr Asn

260 265 270

Ala Lys Asn Arg Thr Glu Asn Ser Glu Arg Glu Arg Asp Val Tyr Glu

275 280 285

Glu Leu Leu Thr Gln Ala Glu Ile Gln Gly Asn Ile Asn Lys Val Asn

290 295 300

Thr Phe Ser Ala Leu Ala Asn Ile Asp Leu Ala Leu Glu Gln Gly Asp

305 310 315 320

Ala Leu Ala Leu Phe Arg Ala Leu Gln Ser Pro Ala Leu Gly Leu Arg

325 330 335

Gly Leu Gln Gln Gln Asn Ser Asp Trp Tyr Leu Lys Gln Leu Leu Ser

340 345 350

Asp Lys Gln Gln Lys Arg Gln Ser Gly Gln Thr Asp Pro Leu Gln Lys

355 360 365

Glu Glu Leu Gln Ser Gly Val Asp Ala Ala Asn Ser Ala Ala Gln Gln

370 375 380

Tyr Gln Arg Arg Leu Ala Ala Val Ala Leu Ile Asn Ala Ala Ile Gln

385 390 395 400

Lys Gly Val Ala Glu Lys Thr Val Leu Glu Leu Met Asn Pro Glu Ala

405 410 415

Gln Leu Pro Gln Val Tyr Pro Phe Ala Ala Asp Leu Tyr Gln Lys Glu

420 425 430

Leu Ala Thr Leu Gln Arg Gln Ser Pro Glu His Asn Leu Thr His Pro

435 440 445

Glu Leu Ser Val Ala Val Glu Met Leu Ser Ser Val Ala Leu Ile Asn

450 455 460

Arg Ala Leu Glu Ser Gly Asp Val Asn Thr Val Trp Lys Gln Leu Ser

465 470 475 480

Ser Ser Val Thr Gly Leu Thr Asn Ile Glu Glu Glu Asn Cys Gln Arg

485 490 495

Tyr Leu Asp Glu Leu Met Lys Leu Lys Ala Gln Ala His Ala Glu Asn

500 505 510

Asn Glu Phe Ile Thr Trp Asn Asp Ile Gln Ala Cys Val Asp His Val

515 520 525

Asn Leu Val Val Gln Glu Glu His Glu Arg Ile Leu Ala Ile Gly Leu

530 535 540

Ile Asn Glu Ala Leu Asp Glu Gly Asp Ala Gln Lys Thr Leu Gln Ala

545 550 555 560

Leu Gln Ile Pro Ala Ala Lys Leu Glu Gly Val Leu Ala Glu Val Ala

565 570 575

Gln His Tyr Gln Asp Thr Leu Ile Arg Ala Lys Arg Glu Lys Ala Gln

580 585 590

Glu Ile Gln Asp Glu Ser Ala Val Leu Trp Leu Asp Glu Ile Gln Gly

595 600 605

Gly Ile Trp Gln Ser Asn Lys Asp Thr Gln Glu Ala Gln Lys Phe Ala

610 615 620

Leu Gly Ile Phe Ala Ile Asn Glu Ala Val Glu Ser Gly Asp Val Gly

625 630 635 640

Lys Thr Leu Ser Ala Leu Arg Ser Pro Asp Val Gly Leu Tyr Gly Val

645 650 655

Ile Pro Glu Cys Gly Glu Thr Tyr His Ser Asp Leu Ala Glu Ala Lys

660 665 670

Lys Lys Lys Leu Ala Val Gly Asp Asn Asn Ser Lys Trp Val Lys His

675 680 685

Trp Val Lys Gly Gly Tyr Tyr Tyr Tyr His Asn Leu Glu Thr Gln Glu

690 695 700

Gly Gly Trp Asp Glu Pro Pro Asn Phe Val Gln Asn Ser Met Gln Leu

705 710 715 720

Ser Arg Glu Glu Ile Gln Ser Ser Ile Ser Gly Val Thr Ala Ala Tyr

725 730 735

Asn Arg Glu Gln Leu Trp Leu Ala Asn Glu Gly Leu Ile Thr Arg Leu

740 745 750

Gln Ala Arg Cys Arg Gly Tyr Leu Val Arg Gln Glu Phe Arg Ser Arg

755 760 765

Met Asn Phe Leu Lys Lys Gln Ile Pro Ala Ile Thr Cys Ile Gln Ser

770 775 780

Gln Trp Arg Gly Tyr Lys Gln Lys Lys Ala Tyr Gln Asp Arg Leu Ala

785 790 795 800

Tyr Leu Arg Ser His Lys Asp Glu Val Val Lys Ile Gln Ser Leu Ala

805 810 815

Arg Met His Gln Ala Arg Lys Arg Tyr Arg Asp Arg Leu Gln Tyr Phe

820 825 830

Arg Asp His Ile Asn Asp Ile Ile Lys Ile Gln Ala Phe Ile Arg Ala

835 840 845

Asn Lys Ala Arg Asp Asp Tyr Lys Thr Leu Ile Asn Ala Glu Asp Pro

850 855 860

Pro Met Val Val Val Arg Lys Phe Val His Leu Leu Asp Gln Ser Asp

865 870 875 880

Gln Asp Phe Gln Glu Glu Leu Asp Leu Met Lys Met Arg Glu Glu Val

885 890 895

Ile Thr Leu Ile Arg Ser Asn Gln Gln Leu Glu Asn Asp Leu Asn Leu

900 905 910

Met Asp Ile Lys Ile Gly Leu Leu Val Lys Asn Lys Ile Thr Leu Gln

915 920 925

Asp Val Val Ser His Ser Lys Lys Leu Thr Lys Lys Asn Lys Glu Gln

930 935 940

Leu Ser Asp Met Met Met Ile Asn Lys Gln Lys Gly Gly Leu Lys Ala

945 950 955 960

Leu Ser Lys Glu Lys Arg Glu Lys Leu Glu Ala Tyr Gln His Leu Phe

965 970 975

Tyr Leu Leu Gln Thr Asn Pro Thr Tyr Leu Ala Lys Leu Ile Phe Gln

980 985 990

Met Pro Gln Asn Lys Ser Thr Lys Phe Met Asp Ser Val Ile Phe Thr

995 1000 1005

Leu Tyr Asn Tyr Ala Ser Asn Gln Arg Glu Glu Tyr Leu Leu Leu

1010 1015 1020

Arg Leu Phe Lys Thr Ala Leu Gln Glu Glu Ile Lys Ser Lys Val

1025 1030 1035

Asp Gln Ile Gln Glu Ile Val Thr Gly Asn Pro Thr Val Ile Lys

1040 1045 1050

Met Val Val Ser Phe Asn Arg Gly Ala Arg Gly Gln Asn Ala Leu

1055 1060 1065

Arg Gln Ile Leu Ala Pro Val Val Lys Glu Ile Met Asp Asp Lys

1070 1075 1080

Ser Leu Asn Ile Lys Thr Asp Pro Val Asp Ile Tyr Lys Ser Trp

1085 1090 1095

Val Asn Gln Met Glu Ser Gln Thr Gly Glu Ala Ser Lys Leu Pro

1100 1105 1110

Tyr Asp Val Thr Pro Glu Gln Ala Leu Ala His Glu Glu Val Lys

1115 1120 1125

Thr Arg Leu Asp Ser Ser Ile Arg Asn Met Arg Ala Val Thr Asp

1130 1135 1140

Lys Phe Leu Ser Ala Ile Val Ser Ser Val Asp Lys Ile Pro Tyr

1145 1150 1155

Gly Met Arg Phe Ile Ala Lys Val Leu Lys Asp Ser Leu His Glu

1160 1165 1170

Lys Phe Pro Asp Ala Gly Glu Asp Glu Leu Leu Lys Ile Ile Gly

1175 1180 1185

Asn Leu Leu Tyr Tyr Arg Tyr Met Asn Pro Ala Ile Val Ala Pro

1190 1195 1200

Asp Ala Phe Asp Ile Ile Asp Leu Ser Ala Gly Gly Gln Leu Thr

1205 1210 1215

Thr Asp Gln Arg Arg Asn Leu Gly Ser Ile Ala Lys Met Leu Gln

1220 1225 1230

His Ala Ala Ser Asn Lys Met Phe Leu Gly Asp Asn Ala His Leu

1235 1240 1245

Ser Ile Ile Asn Glu Tyr Leu Ser Gln Ser Tyr Gln Lys Phe Arg

1250 1255 1260

Arg Phe Phe Gln Thr Ala Cys Asp Val Pro Glu Leu Gln Asp Lys

1265 1270 1275

Phe Asn Val Asp Glu Tyr Ser Asp Leu Val Thr Leu Thr Lys Pro

1280 1285 1290

Val Ile Tyr Ile Ser Ile Gly Glu Ile Ile Asn Thr His Thr Leu

1295 1300 1305

Leu Leu Asp His Gln Asp Ala Ile Ala Pro Glu His Asn Asp Pro

1310 1315 1320

Ile His Glu Leu Leu Asp Asp Leu Gly Glu Val Pro Thr Ile Glu

1325 1330 1335

Ser Leu Ile Gly Glu Ser Ser Gly Asn Leu Asn Asp Pro Asn Lys

1340 1345 1350

Glu Ala Leu Ala Lys Thr Glu Val Ser Leu Thr Leu Thr Asn Lys

1355 1360 1365

Phe Asp Val Pro Gly Asp Glu Asn Ala Glu Met Asp Ala Arg Thr

1370 1375 1380

Ile Leu Leu Asn Thr Lys Arg Leu Ile Val Asp Val Ile Arg Phe

1385 1390 1395

Gln Pro Gly Glu Thr Leu Thr Glu Ile Leu Glu Thr Pro Ala Thr

1400 1405 1410

Ser Glu Gln Glu Ala Glu His Gln Arg Ala Met Gln Arg Arg Ala

1415 1420 1425

Ile Arg Asp Ala Lys Thr Pro Asp Lys Met Lys Lys Ser Lys Ser

1430 1435 1440

Val Lys Glu Asp Ser Asn Leu Thr Leu Gln Glu Lys Lys Glu Lys

1445 1450 1455

Ile Gln Thr Gly Leu Lys Lys Leu Thr Glu Leu Gly Thr Val Asp

1460 1465 1470

Pro Lys Asn Lys Tyr Gln Glu Leu Ile Asn Asp Ile Ala Arg Asp

1475 1480 1485

Ile Arg Asn Gln Arg Arg Tyr Arg Gln Arg Arg Lys Ala Glu Leu

1490 1495 1500

Val Lys Leu Gln Gln Thr Tyr Ala Ala Leu Asn Ser Lys Ala Thr

1505 1510 1515

Phe Tyr Gly Glu Gln Val Asp Tyr Tyr Lys Ser Tyr Ile Lys Thr

1520 1525 1530

Cys Leu Asp Asn Leu Ala Ser Lys Gly Lys Val Ser Lys Lys Pro

1535 1540 1545

Arg Glu Met Lys Gly Lys Lys Ser Lys Lys Ile Ser Leu Lys Tyr

1550 1555 1560

Thr Ala Ala Arg Leu His Glu Lys Gly Val Leu Leu Glu Ile Glu

1565 1570 1575

Asp Leu Gln Val Asn Gln Phe Lys Asn Val Ile Phe Glu Ile Ser

1580 1585 1590

Pro Thr Glu Glu Val Gly Asp Phe Glu Val Lys Ala Lys Phe Met

1595 1600 1605

Gly Val Gln Met Glu Thr Phe Met Leu His Tyr Gln Asp Leu Leu

1610 1615 1620

Gln Leu Gln Tyr Glu Gly Val Ala Val Met Lys Leu Phe Asp Arg

1625 1630 1635

Ala Lys Val Asn Val Asn Leu Leu Ile Phe Leu Leu Asn Lys Lys

1640 1645 1650

Phe Tyr Gly Lys

1655

<210> 26

<211> 627

<212> PRT

<213> Homo sapiens

<220>

<221> L-plastin (Lymphocyte cytosolic protein 1)

<222> (1)..(627)

<223> swissprot accession No. as of 09 Dec 2002: P13796

<400> 26

Met Ala Arg Gly Ser Val Ser Asp Glu Glu Met Met Glu Leu Arg Glu
1 5 10 15

Ala Phe Ala Lys Val Asp Thr Asp Gly Asn Gly Tyr Ile Ser Phe Asn
20 25 30

Glu Leu Asn Asp Leu Phe Lys Ala Ala Cys Leu Pro Leu Pro Gly Tyr
35 40 45

Arg Val Arg Glu Ile Thr Glu Asn Leu Met Ala Thr Gly Asp Leu Asp
50 55 60

Gln Asp Gly Arg Ile Ser Phe Asp Glu Phe Ile Lys Ile Phe His Gly
65 70 75 80

Leu Lys Ser Thr Asp Val Ala Lys Thr Phe Arg Lys Ala Ile Asn Lys
85 90 95

Lys Glu Gly Ile Cys Ala Ile Gly Gly Thr Ser Glu Gln Ser Ser Val
100 105 110

Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala Phe Val Asn
115 120 125

Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg His Val Ile
130 135 140

Pro Met Asn Pro Asn Thr Asn Asp Leu Phe Asn Ala Val Gly Asp Gly
145 150 155 160

Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp Thr Ile Asp
165 170 175

Glu Arg Thr Ile Asn Lys Lys Lys Leu Thr Pro Phe Thr Ile Gln Glu
180 185 190

Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly Cys His Val
195 200 205

Val Asn Ile Gly Ala Glu Asp Leu Lys Glu Gly Lys Pro Tyr Leu Val
210 215 220

Leu Gly Leu Leu Trp Gln Val Ile Lys Ile Gly Leu Phe Ala Asp Ile
225 230 235 240

Glu Leu Ser Arg Asn Glu Ala Leu Ile Ala Leu Leu Arg Glu Gly Glu
245 250 255

Ser Leu Glu Asp Leu Met Lys Leu Ser Pro Glu Glu Leu Leu Leu Arg
260 265 270

Trp Ala Asn Tyr His Leu Glu Asn Ala Gly Cys Asn Lys Ile Gly Asn
275 280 285

Phe Ser Thr Asp Ile Lys Asp Ser Lys Ala Tyr Tyr His Leu Leu Glu
290 295 300

Gln Val Ala Pro Lys Gly Asp Glu Glu Gly Val Pro Ala Val Val Ile
305 310 315 320

Asp Met Ser Gly Leu Arg Glu Lys Asp Asp Ile Gln Arg Ala Glu Cys
325 330 335
Met Leu Gln Gln Ala Glu Arg Leu Gly Cys Arg Gln Phe Val Thr Ala
340 345 350
Thr Asp Val Val Arg Gly Asn Pro Lys Leu Asn Leu Ala Phe Ile Ala
355 360 365
Asn Leu Phe Asn Arg Tyr Pro Ala Leu His Lys Pro Glu Asn Gln Asp
370 375 380
Ile Asp Trp Gly Ala Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe
385 390 395 400
Arg Asn Trp Met Asn Ser Leu Gly Val Asn Pro Arg Val Asn His Leu
405 410 415
Tyr Ser Asp Leu Ser Asp Ala Leu Val Ile Phe Gln Leu Tyr Glu Lys
420 425 430
Ile Lys Val Pro Val Asp Trp Asn Arg Val Asn Lys Pro Pro Tyr Pro
435 440 445
Lys Leu Gly Gly Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val
450 455 460
Glu Leu Gly Lys Asn Gln Ala Lys Phe Ser Leu Val Gly Ile Gly Gly
465 470 475 480
Gln Asp Leu Asn Glu Gly Asn Arg Thr Leu Thr Leu Ala Leu Ile Trp
485 490 495
Gln Leu Met Arg Arg Tyr Thr Leu Asn Ile Leu Glu Glu Ile Gly Gly
500 505 510
Gly Gln Lys Val Asn Asp Asp Ile Ile Val Asn Trp Val Asn Glu Thr
515 520 525

Leu Arg Glu Ala Glu Lys Ser Ser Ser Ile Ser Ser Phe Lys Asp Pro
530 535 540

Lys Ile Ser Thr Ser Leu Pro Val Leu Asp Leu Ile Asp Ala Ile Gln
545 550 555 560

Pro Gly Ser Ile Asn Tyr Asp Leu Leu Lys Thr Glu Asn Leu Asn Asp
565 570 575

Asp Glu Lys Leu Asn Asn Ala Lys Tyr Ala Ile Ser Met Ala Arg Lys
580 585 590

Ile Gly Ala Arg Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Asn
595 600 605

Pro Lys Met Val Met Thr Val Phe Ala Cys Leu Met Gly Lys Gly Met
610 615 620

Lys Arg Val
625

<210> 27
<211> 216
<212> PRT
<213> Homo sapiens
<220>
<221> GTP-binding nuclear protein RAN
<222> (1)..(216)
<223> swissprot accession No. as of 09 Dec 2002: P17080

<400> 27

Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
1 5 10 15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
20 25 30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
35 40 45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
50 55 60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65 70 75 80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
85 90 95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
100 105 110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
115 120 125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
130 135 140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145 150 155 160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
165 170 175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
180 185 190
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala

195 200 205

Leu Pro Asp Glu Asp Asp Asp Leu

210 215

<210> 28

<211> 463

<212> PRT

<213> Homo sapiens

<220>

<221> Heterogeneous nuclear ribonucleoprotein K

<222> (1)..(463)

<223> swissprot accession No. as of 09 Dec 2002: Q07244

<400> 28

Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn

1 5 10 15

Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala

20 25 30

Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu

35 40 45

Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn

50 55 60

Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp

65 70 75 80

Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
85 90 95

Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
100 105 110

Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
115 120 125

Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
130 135 140

Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
145 150 155 160

Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
165 170 175

Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
180 185 190

Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
195 200 205

Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
210 215 220

Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
225 230 235 240

Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
245 250 255

Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
260 265 270

Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
275 280 285

Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
290 295 300

Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
305 310 315 320

Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
325 330 335

Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
340 345 350

Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
355 360 365

Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
370 375 380

Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
385 390 395 400

Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
405 410 415

Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
420 425 430

Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
435 440 445

Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
450 455 460

<210> 29

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> Translationally controlled tumor protein (TCTP)

<222> (1)..(172)

<223> swissprot accession No. as of 09 Dec 2002: P13693

<400> 29

```
Met Ile Ile Tyr Arg Asp Leu Ile Ser His Asp Glu Met Phe Ser Asp
1               5                  10                  15
Ile Tyr Lys Ile Arg Glu Ile Ala Asp Gly Leu Cys Leu Glu Val Glu
            20                  25                  30
Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
        35                  40                  45
Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
    50                  55                  60
Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
65                  70                  75                  80
Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
                85                  90                  95
Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
            100                 105                 110
Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
        115                 120                 125
Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
```

130 135 140

Met Val Ala Leu Leu Asp Tyr Arg Glu Asp Gly Val Thr Pro Tyr Met

145 150 155 160

Ile Phe Phe Lys Asp Gly Leu Glu Met Glu Lys Cys

165 170

<210> 30

<211> 284

<212> PRT

<213> Homo sapiens

<220>

<221> Tropomyosin 1 alpha chain

<222> (1)..(284)

<223> swissprot accession No. P09493

<400> 30

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu

1 5 10 15

Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala

20 25 30

Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys

35 40 45

Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu

50 55 60

Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
65 70 75 80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
85 90 95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys
100 105 110
Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys
115 120 125
Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln
130 135 140
Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg
145 150 155 160
Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu
165 170 175
Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu
180 185 190
Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu
195 200 205
Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Arg Tyr Glu Glu Glu
210 215 220
Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu
225 230 235 240
Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu
245 250 255
Glu Asp Glu Leu Tyr Ala Gln Lys Leu Lys Tyr Lys Ala Ile Ser Glu
260 265 270

Glu Leu Asp His Ala Leu Asn Asp Met Thr Ser Ile

275 280

<210> 31

<211> 482

<212> PRT

<213> Homo sapiens

<220>

<221> Thymidine phosphorylase precursor

<222> (1)..(482)

<223> swissprot accession No. as of 09 Dec 2002: P19971

<400> 31

Met Ala Ala Leu Met Thr Pro Gly Thr Gly Ala Pro Pro Ala Pro Gly

1 5 10 15

Asp Phe Ser Gly Glu Gly Ser Gln Gly Leu Pro Asp Pro Ser Pro Glu

20 25 30

Pro Lys Gln Leu Pro Glu Leu Ile Arg Met Lys Arg Asp Gly Gly Arg

35 40 45

Leu Ser Glu Ala Asp Ile Arg Gly Phe Val Ala Ala Val Val Asn Gly

50 55 60

Ser Ala Gln Gly Ala Gln Ile Gly Ala Met Leu Met Ala Ile Arg Leu

65 70 75 80

Arg Gly Met Asp Leu Glu Glu Thr Ser Val Leu Thr Gln Ala Leu Ala

85 90 95

Gln Ser Gly Gln Gln Leu Glu Trp Pro Glu Ala Trp Arg Gln Gln Leu
100 105 110
Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Lys Val Ser Leu Val
115 120 125
Leu Ala Pro Ala Leu Ala Ala Cys Gly Cys Lys Val Pro Met Ile Ser
130 135 140
Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu Ser
145 150 155 160
Ile Pro Gly Phe Asn Val Ile Gln Ser Pro Glu Gln Met Gln Val Leu
165 170 175
Leu Asp Gln Ala Gly Cys Cys Ile Val Gly Gln Ser Glu Gln Leu Val
180 185 190
Pro Ala Asp Gly Ile Leu Tyr Ala Ala Arg Asp Val Thr Ala Thr Val
195 200 205
Asp Ser Leu Pro Leu Ile Thr Ala Ser Ile Leu Ser Lys Lys Leu Val
210 215 220
Glu Gly Leu Ser Ala Leu Val Val Asp Val Lys Phe Gly Gly Ala Ala
225 230 235 240
Val Phe Pro Asn Gln Glu Gln Ala Arg Glu Leu Ala Lys Thr Leu Val
245 250 255
Gly Val Gly Ala Ser Leu Gly Leu Arg Val Ala Ala Ala Leu Thr Ala
260 265 270
Met Asp Lys Pro Leu Gly Arg Cys Val Gly His Ala Leu Glu Val Glu
275 280 285
Glu Ala Leu Leu Cys Met Asp Gly Ala Gly Pro Pro Asp Leu Arg Asp
290 295 300

Leu Val Thr Thr Leu Gly Gly Ala Leu Leu Trp Leu Ser Gly His Ala
305 310 315 320
Gly Thr Gln Ala Gln Gly Ala Ala Arg Val Ala Ala Ala Leu Asp Asp
325 330 335
Gly Ser Ala Leu Gly Arg Phe Glu Arg Met Leu Ala Ala Gln Gly Val
340 345 350
Asp Pro Gly Leu Ala Arg Ala Leu Cys Ser Gly Ser Pro Ala Glu Arg
355 360 365
Arg Gln Leu Leu Pro Arg Ala Arg Glu Gln Glu Glu Leu Leu Ala Pro
370 375 380
Ala Asp Gly Thr Val Glu Leu Val Arg Ala Leu Pro Leu Ala Leu Val
385 390 395 400
Leu His Glu Leu Gly Ala Gly Arg Ser Arg Ala Gly Glu Pro Leu Arg
405 410 415
Leu Gly Val Gly Ala Glu Leu Leu Val Asp Val Gly Gln Arg Leu Arg
420 425 430
Arg Gly Thr Pro Trp Leu Arg Val His Arg Asp Gly Pro Ala Leu Ser
435 440 445
Gly Pro Gln Ser Arg Ala Leu Gln Glu Ala Leu Val Leu Ser Asp Arg
450 455 460
Ala Pro Phe Ala Ala Pro Leu Pro Phe Ala Glu Leu Val Leu Pro Pro
465 470 475 480
Gln Gln

<210> 32

<211> 488

<212> PRT

<213> Homo sapiens

<220>

<221> Cytosol aminopeptidase

<222> (1)..(488)

<223> swissprot accession No. as of 09 Dec 2002: P28838

<400> 32

Met Thr Lys Gly Leu Val Leu Gly Ile Tyr Ser Lys Glu Lys Glu Asp
1 5 10 15
Asp Val Pro Gln Phe Thr Ser Ala Gly Glu Asn Phe Asp Lys Leu Leu
20 25 30
Ala Gly Lys Leu Arg Glu Thr Leu Asn Ile Ser Gly Pro Pro Leu Lys
35 40 45
Ala Gly Lys Thr Arg Thr Phe Tyr Gly Leu His Gln Asp Phe Pro Ser
50 55 60
Val Val Leu Val Gly Leu Gly Lys Lys Ala Ala Gly Ile Asp Glu Gln
65 70 75 80
Glu Asn Trp His Glu Gly Lys Glu Asn Ile Arg Ala Ala Val Ala Ala
85 90 95
Gly Cys Arg Gln Ile Gln Asp Leu Glu Leu Ser Ser Val Glu Val Asp
100 105 110
Pro Cys Gly Asp Ala Gln Ala Ala Ala Glu Gly Ala Val Leu Gly Leu

115 120 125

Tyr Glu Tyr Asp Asp Leu Lys Gln Lys Lys Lys Met Ala Val Ser Ala

130 135 140

Lys Leu Tyr Gly Ser Gly Asp Gln Glu Ala Trp Gln Lys Gly Val Leu

145 150 155 160

Phe Ala Ser Gly Gln Asn Leu Ala Arg Gln Leu Met Glu Thr Pro Ala

165 170 175

Asn Glu Met Thr Pro Thr Arg Phe Ala Glu Ile Ile Glu Lys Asn Leu

180 185 190

Lys Ser Ala Ser Ser Lys Thr Glu Val His Ile Arg Pro Lys Ser Trp

195 200 205

Ile Glu Glu Gln Ala Met Gly Ser Phe Leu Ser Val Ala Lys Gly Ser

210 215 220

Asp Glu Pro Pro Val Phe Leu Glu Ile His Tyr Lys Gly Ser Pro Asn

225 230 235 240

Ala Asn Glu Pro Pro Leu Val Phe Val Gly Lys Gly Ile Thr Phe Asp

245 250 255

Ser Gly Gly Ile Ser Ile Lys Ala Ser Ala Asn Met Asp Leu Met Arg

260 265 270

Ala Asp Met Gly Gly Ala Ala Thr Ile Cys Ser Ala Ile Val Ser Ala

275 280 285

Ala Lys Leu Asn Leu Pro Ile Asn Ile Ile Gly Leu Ala Pro Leu Cys

290 295 300

Glu Asn Met Pro Ser Gly Lys Ala Asn Lys Pro Gly Asp Val Val Arg

305 310 315 320

Ala Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly

325 330 335

Arg Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro

340 345 350

Lys Val Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala

355 360 365

Leu Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp

370 375 380

Asn Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg

385 390 395 400

Met Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu

405 410 415

Ala Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr

420 425 430

Ala Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His

435 440 445

Leu Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu

450 455 460

Arg Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu

465 470 475 480

Leu Arg Phe Ser Gln Asp Asn Ala

485

<210> 33

<211> 400

<212> PRT

<213> Homo sapiens

<220>

<221> Keratin, type I cytoskeletal 19

<222> (1)..(400)

<223> swissprot accession No. as of 09 Dec 2002 : P08727

<400> 33

Met Thr Ser Tyr Ser Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly
1 5 10 15

Gly Leu Gly Gly Gly Ser Val Arg Phe Gly Pro Gly Val Ala Phe Arg
20 25 30

Ala Pro Ser Ile His Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser
35 40 45

Ser Ala Arg Phe Val Ser Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly
50 55 60

Tyr Gly Gly Val Leu Thr Ala Ser Asp Gly Leu Leu Ala Gly Asn Glu
65 70 75 80

Lys Leu Thr Met Gln Asn Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp
85 90 95

Lys Val Arg Ala Leu Glu Ala Ala Asn Gly Glu Leu Glu Val Lys Ile
100 105 110

Arg Asp Trp Tyr Gln Lys Gln Gly Pro Gly Pro Ser Arg Asp Tyr Ser
115 120 125

His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys Ile Leu Gly Ala
130 135 140

Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
145 150 155 160
Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
165 170 175
Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu
180 185 190
Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile Glu Gly Leu Lys
195 200 205
Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Ile Ser Thr
210 215 220
Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Glu Val Asp Ser Ala
225 230 235 240
Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met Arg Ser Gln Tyr
245 250 255
Glu Val Met Ala Glu Gln Asn Arg Lys Asp Ala Glu Ala Trp Phe Thr
260 265 270
Ser Arg Thr Glu Glu Leu Asn Arg Glu Val Ala Gly His Thr Glu Gln
275 280 285
Leu Gln Met Ser Arg Ser Glu Val Thr Asp Leu Arg Arg Thr Leu Gln
290 295 300
Gly Leu Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ala Leu
305 310 315 320
Glu Asp Thr Leu Ala Glu Thr Glu Ala Arg Phe Gly Ala Gln Leu Ala
325 330 335
His Ile Gln Ala Leu Ile Ser Gly Ile Glu Ala Gln Leu Ala Asp Val
340 345 350

Arg Ala Asp Ser Glu Arg Gln Asn Gln Glu Tyr Gln Arg Leu Met Asp
355 360 365

Ile Lys Ser Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Ser Leu Leu
370 375 380

Glu Gly Gln Glu Asp His Tyr Asn Asn Leu Ser Ala Ser Lys Val Leu
385 390 395 400

<210> 34

<211> 325

<212> PRT

<213> Homo sapiens

<220>

<221> Alcohol dehydrogenase [NADP+]

<222> (1)..(325)

<223> swissprot accession No. as of 09 Dec 2002: P14550

<400> 34

Met Ala Ala Ser Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu
1 5 10 15

Ile Gly Leu Gly Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala
20 25 30

Val Lys Tyr Ala Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala
35 40 45

Ile Tyr Gly Asn Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val

50 55 60

Gly Pro Gly Lys Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys

65 70 75 80

Leu Trp Asn Thr Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg

85 90 95

Lys Thr Leu Ala Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met

100 105 110

His Trp Pro Tyr Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn

115 120 125

Ala Asp Gly Thr Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp

130 135 140

Lys Ala Leu Glu Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly

145 150 155 160

Leu Ser Asn Phe Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala

165 170 175

Ser Val Arg Pro Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala

180 185 190

Gln Asn Glu Leu Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr

195 200 205

Ala Tyr Ser Pro Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp

210 215 220

Glu Pro Val Leu Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys

225 230 235 240

Tyr Gly Arg Ser Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg

245 250 255

Lys Val Ile Cys Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln

260 265 270

Asn Ile Lys Val Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln

275 280 285

Leu Asn Ala Leu Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr

290 295 300

Val Asp Gly Lys Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro

305 310 315 320

Phe Asn Asp Pro Tyr

325

<210> 35

<211> 270

<212> PRT

<213> Homo sapiens

<220>

<221> Elastase IIIA precursor

<222> (1)..(270)

<223> swissprot accession No. as of 09 Dec 2002: P09093

<400> 35

Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser

1 5 10 15

Gly Tyr Gly Pro Pro Ser Ser His Ser Ser Ser Arg Val Val His Gly

20 25 30

Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
35 40 45
Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
50 55 60
Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr
65 70 75 80
Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro
85 90 95
Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu
100 105 110
Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
115 120 125
Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
130 135 140
Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr
145 150 155 160
Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
165 170 175
Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn
180 185 190
Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr
195 200 205
Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
210 215 220
Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
225 230 235 240

Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val
245 250 255

Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His
260 265 270

<210> 36

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> Dihydrolipoamide dehydrogenase, mitochondrial precursor

<222> (1)..(509)

<223> swissprot accession No. as of 09 Dec 2002: P09622

<400> 36

Met Gln Ser Trp Ser Arg Val Tyr Cys Ser Leu Ala Lys Arg Gly His
1 5 10 15

Phe Asn Arg Ile Ser His Gly Leu Gln Gly Leu Ser Ala Val Pro Leu
20 25 30

Arg Thr Tyr Ala Asp Gln Pro Ile Asp Ala Asp Val Thr Val Ile Gly
35 40 45

Ser Gly Pro Gly Gly Tyr Val Ala Ala Ile Lys Ala Ala Gln Leu Gly
50 55 60

Phe Lys Thr Val Cys Ile Glu Lys Asn Glu Thr Leu Gly Gly Thr Cys

65 70 75 80

Leu Asn Val Gly Cys Ile Pro Ser Lys Ala Leu Leu Asn Asn Ser His

85 90 95

Tyr Tyr His Met Ala His Gly Thr Asp Phe Ala Ser Arg Gly Ile Glu

100 105 110

Met Ser Glu Val Arg Leu Asn Leu Asp Lys Met Met Glu Gln Lys Ser

115 120 125

Thr Ala Val Lys Ala Leu Thr Gly Gly Ile Ala His Leu Phe Lys Gln

130 135 140

Asn Lys Val Val His Val Asn Gly Tyr Gly Lys Ile Thr Gly Lys Asn

145 150 155 160

Gln Val Thr Ala Thr Lys Ala Asp Gly Gly Thr Gln Val Ile Asp Thr

165 170 175

Lys Asn Ile Leu Ile Ala Thr Gly Ser Glu Val Thr Pro Phe Pro Gly

180 185 190

Ile Thr Ile Asp Glu Asp Thr Ile Val Ser Ser Thr Gly Ala Leu Ser

195 200 205

Leu Lys Lys Val Pro Glu Lys Met Val Val Ile Gly Ala Gly Val Ile

210 215 220

Gly Val Glu Leu Gly Ser Val Trp Gln Arg Leu Gly Ala Asp Val Thr

225 230 235 240

Ala Val Glu Phe Leu Gly His Val Gly Gly Val Gly Ile Asp Met Glu

245 250 255

Ile Ser Lys Asn Phe Gln Arg Ile Leu Gln Lys Gln Gly Phe Lys Phe

260 265 270

Lys Leu Asn Thr Lys Val Thr Gly Ala Thr Lys Lys Ser Asp Gly Lys

275 280 285

Ile Asp Val Ser Ile Glu Ala Ala Ser Gly Gly Lys Ala Glu Val Ile

290 295 300

Thr Cys Asp Val Leu Leu Val Cys Ile Gly Arg Arg Pro Phe Thr Lys

305 310 315 320

Asn Leu Gly Leu Glu Glu Leu Gly Ile Glu Leu Asp Pro Arg Gly Arg

325 330 335

Ile Pro Val Asn Thr Arg Phe Gln Thr Lys Ile Pro Asn Ile Tyr Ala

340 345 350

Ile Gly Asp Val Val Ala Gly Pro Met Leu Ala His Lys Ala Glu Asp

355 360 365

Glu Gly Ile Ile Cys Val Glu Gly Met Ala Gly Gly Ala Val His Ile

370 375 380

Asp Tyr Asn Cys Val Pro Ser Val Ile Tyr Thr His Pro Glu Val Ala

385 390 395 400

Trp Val Gly Lys Ser Glu Glu Gln Leu Lys Glu Glu Gly Ile Glu Tyr

405 410 415

Lys Val Gly Lys Phe Pro Phe Ala Ala Asn Ser Arg Ala Lys Thr Asn

420 425 430

Ala Asp Thr Asp Gly Met Val Lys Ile Leu Gly Gln Lys Ser Thr Asp

435 440 445

Arg Val Leu Gly Ala His Ile Leu Gly Pro Gly Ala Gly Glu Met Val

450 455 460

Asn Glu Ala Ala Leu Ala Leu Glu Tyr Gly Ala Ser Cys Glu Asp Ile

465 470 475 480

Ala Arg Val Cys His Ala His Pro Thr Leu Ser Glu Ala Phe Arg Glu

485 490 495

Ala Asn Leu Ala Ala Ser Phe Gly Lys Ser Ile Asn Phe

500 505

<210> 37

<211> 290

<212> PRT

<213> Homo sapiens

<220>

<221> Enoyl-CoA hydratase, mitochondrial precursor

<222> (1)..(290)

<223> swissprot accession No. as of 09 Dec 2002: P30084

<400> 37

Met Ala Ala Leu Arg Val Leu Leu Ser Cys Ala Arg Gly Pro Leu Arg
1 5 10 15

Pro Pro Val Arg Cys Pro Ala Trp Arg Pro Phe Ala Ser Gly Ala Asn
20 25 30

Phe Glu Tyr Ile Ile Ala Glu Lys Arg Gly Lys Asn Asn Thr Val Gly
35 40 45

Leu Ile Gln Leu Asn Arg Pro Lys Ala Leu Asn Ala Leu Cys Asp Gly
50 55 60

Leu Ile Asp Glu Leu Asn Gln Ala Leu Lys Ile Phe Glu Glu Asp Pro
65 70 75 80

Ala Val Gly Ala Ile Val Leu Thr Gly Gly Asp Lys Ala Phe Ala Ala
85 90 95

Gly Ala Asp Ile Lys Glu Met Gln Asn Leu Ser Phe Gln Asp Cys Tyr
100 105 110

Ser Ser Lys Phe Leu Lys His Trp Asp His Leu Thr Gln Val Lys Lys
115 120 125

Pro Val Ile Ala Ala Val Asn Gly Tyr Ala Phe Gly Gly Gly Cys Glu
130 135 140

Leu Ala Met Met Cys Asp Ile Ile Tyr Ala Gly Glu Lys Ala Gln Phe
145 150 155 160

Ala Gln Pro Glu Ile Leu Ile Gly Thr Ile Pro Gly Ala Gly Gly Thr
165 170 175

Gln Arg Leu Thr Arg Ala Val Gly Lys Ser Leu Ala Met Glu Met Val
180 185 190

Leu Thr Gly Asp Arg Ile Ser Ala Gln Asp Ala Lys Gln Ala Gly Leu
195 200 205

Val Ser Lys Ile Cys Pro Val Glu Thr Leu Val Glu Glu Ala Ile Gln
210 215 220

Cys Ala Glu Lys Ile Ala Ser Asn Ser Lys Ile Val Val Ala Met Ala
225 230 235 240

Lys Glu Ser Val Asn Ala Ala Phe Glu Met Thr Leu Thr Glu Gly Ser
245 250 255

Lys Leu Glu Lys Lys Leu Phe Tyr Ser Thr Phe Ala Thr Asp Asp Arg
260 265 270

Lys Glu Gly Met Thr Ala Phe Val Glu Lys Arg Lys Ala Asn Phe Lys
275 280 285

Asp Gln

290

<210> 38

<211> 160

<212> PRT

<213> Homo sapiens

<220>

<221> Heat-shock 20 kDa like-protein p20

<222> (1)..(160)

<223> swissprot accession No. as of 09 Dec 2002: O14558

<400> 38

Met Glu Ile Pro Val Pro Val Gln Pro Ser Trp Leu Arg Arg Ala Ser
1 5 10 15
Ala Pro Leu Pro Gly Leu Ser Ala Pro Gly Arg Leu Phe Asp Gln Arg
20 25 30
Phe Gly Glu Gly Leu Leu Glu Ala Glu Leu Ala Ala Leu Cys Pro Thr
35 40 45
Thr Leu Ala Pro Tyr Tyr Leu Arg Ala Pro Ser Val Ala Leu Pro Val
50 55 60
Ala Gln Val Pro Thr Asp Pro Gly His Phe Ser Val Leu Leu Asp Val
65 70 75 80
Lys His Phe Ser Pro Glu Glu Ile Ala Val Lys Val Val Gly Glu His

85 90 95

Val Glu Val His Ala Arg His Glu Glu Arg Pro Asp Glu His Gly Phe

100 105 110

Val Ala Arg Glu Phe His Arg Arg Tyr Arg Leu Pro Pro Gly Val Asp

115 120 125

Pro Ala Ala Val Thr Ser Ala Leu Ser Pro Glu Gly Val Leu Ser Ile

130 135 140

Gln Ala Ala Pro Ala Ser Ala Gln Ala Pro Pro Pro Ala Ala Ala Lys

145 150 155 160

<210> 39

<211> 151

<212> PRT

<213> Homo sapiens

<220>

<221> Myosin light chain alkali, non-muscle isoform

<222> (1)..(151)

<223> swissprot accession No. as of 09 Dec 2002: P16475

<400> 39

Met Cys Asp Phe Thr Glu Asp Gln Thr Ala Glu Phe Lys Glu Ala Phe

1 5 10 15

Gln Leu Phe Asp Arg Thr Gly Asp Gly Lys Ile Leu Tyr Ser Gln Cys

20 25 30

Gly Asp Val Met Arg Ala Leu Gly Gln Asn Pro Thr Asn Ala Glu Val
35 40 45
Leu Lys Val Leu Gly Asn Pro Lys Ser Asp Glu Met Asn Val Lys Val
50 55 60
Leu Asp Phe Glu His Phe Leu Pro Met Leu Gln Thr Val Ala Lys Asn
65 70 75 80
Lys Asp Gln Gly Thr Tyr Glu Asp Tyr Val Glu Gly Leu Arg Val Phe
85 90 95
Asp Lys Glu Gly Asn Gly Thr Val Met Gly Ala Glu Ile Arg His Val
100 105 110
Leu Val Thr Leu Gly Glu Lys Met Thr Glu Glu Glu Val Glu Met Leu
115 120 125
Val Ala Gly His Glu Asp Ser Asn Gly Cys Ile Asn Tyr Glu Ala Phe
130 135 140
Val Arg His Ile Leu Ser Gly
145 150

<210> 40
<211> 592
<212> PRT
<213> Homo sapiens
<220>
<221> Calnexin precursor
<222> (1)..(592)
<223> swissprot accession No. as of 09 Dec 2002: P27824

<400> 40

Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala
1 5 10 15

Ile Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu
20 25 30

Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp
35 40 45

Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val
50 55 60

Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu
65 70 75 80

Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu
85 90 95

Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser
100 105 110

Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His
115 120 125

His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys
130 135 140

Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys
145 150 155 160

Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu
165 170 175

Asp Gln Phe His Asp Lys Thr Pro Tyr Thr Ile Met Phe Gly Pro Asp

180 185 190

Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn

195 200 205

Pro Lys Thr Gly Ile Tyr Glu Glu Lys His Ala Lys Arg Pro Asp Ala

210 215 220

Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu

225 230 235 240

Ile Leu Asn Pro Asp Asn Ser Phe Glu Ile Leu Val Asp Gln Ser Val

245 250 255

Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro

260 265 270

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp

275 280 285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp

290 295 300

Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro

305 310 315 320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala

325 330 335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala

340 345 350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val

355 360 365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys

370 375 380

Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg

385 390 395 400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met

405 410 415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp

420 425 430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp

435 440 445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala

450 455 460

Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg

465 470 475 480

Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe

485 490 495

Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Lys Gln Thr Ser Gly Met

500 505 510

Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu

515 520 525

Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly

530 535 540

Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly

545 550 555 560

Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu

565 570 575

Asp Glu Ile Leu Asn Arg Ser Pro Arg Asn Arg Lys Pro Arg Arg Glu

580 585 590

<210> 41

<211> 282

<212> PRT

<213> Homo sapiens

<220>

<221> Complement component 1

<222> (1)..(282)

<223> swissprot accession No. as of 09 Dec 2002

<400> 41

Met Leu Pro Leu Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val
1 5 10 15

Ala Gly Leu Arg Ala Ala Ala Pro Ala Ser Pro Phe Arg Gln Leu Leu
20 25 30

Gln Pro Ala Pro Arg Leu Cys Thr Arg Pro Phe Gly Leu Leu Ser Val
35 40 45

Arg Ala Gly Ser Glu Arg Arg Pro Gly Leu Leu Arg Pro Arg Gly Pro
50 55 60

Cys Ala Cys Gly Cys Gly Cys Gly Ser Leu His Thr Asp Gly Asp Lys
65 70 75 80

Ala Phe Val Asp Phe Leu Ser Asp Glu Ile Lys Glu Glu Arg Lys Ile
85 90 95

Gln Lys His Lys Thr Leu Pro Lys Met Ser Gly Gly Trp Glu Leu Glu

100 105 110

Leu Asn Gly Thr Glu Ala Lys Leu Val Arg Lys Val Ala Gly Glu Lys

115 120 125

Ile Thr Val Thr Phe Asn Ile Asn Asn Ser Ile Pro Pro Thr Phe Asp

130 135 140

Gly Glu Glu Glu Pro Ser Gln Gly Gln Lys Val Glu Glu Gln Glu Pro

145 150 155 160

Glu Leu Thr Ser Thr Pro Asn Phe Val Val Glu Val Ile Lys Asn Asp

165 170 175

Asp Gly Lys Lys Ala Leu Val Leu Asp Cys His Tyr Pro Glu Asp Glu

180 185 190

Val Gly Gln Glu Asp Glu Ala Glu Ser Asp Ile Phe Ser Ile Arg Glu

195 200 205

Val Ser Phe Gln Ser Thr Gly Glu Ser Glu Trp Lys Asp Thr Asn Tyr

210 215 220

Thr Leu Asn Thr Asp Ser Leu Asp Trp Ala Leu Tyr Asp His Leu Met

225 230 235 240

Asp Phe Leu Ala Asp Arg Gly Val Asp Asn Thr Phe Ala Asp Glu Leu

245 250 255

Val Glu Leu Ser Thr Ala Leu Glu His Gln Glu Tyr Ile Thr Phe Leu

260 265 270

Glu Asp Leu Lys Ser Phe Val Lys Ser Gln

275 280

<210> 42

<211> 727

<212> PRT

<213> Homo sapiens

<220>

<221> NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor

<222> (1)..(727)

<223> swissprot accession No. as of 09 Dec 2002: P28331

<400> 42

Met Leu Arg Ile Pro Val Arg Arg Ala Leu Val Gly Leu Ser Lys Ser
1 5 10 15
Pro Lys Gly Cys Val Arg Thr Thr Ala Thr Ala Ala Ser Asn Leu Ile
20 25 30
Glu Val Phe Val Asp Gly Gln Ser Val Met Val Glu Pro Gly Thr Thr
35 40 45
Val Leu Gln Ala Cys Glu Lys Val Gly Met Gln Ile Pro Arg Phe Cys
50 55 60
Tyr His Glu Arg Leu Ser Val Ala Gly Asn Cys Arg Met Cys Leu Val
65 70 75 80
Glu Ile Glu Lys Ala Pro Lys Val Val Ala Ala Cys Ala Met Pro Val
85 90 95
Met Lys Gly Trp Asn Ile Leu Thr Asn Ser Glu Lys Ser Lys Lys Ala
100 105 110
Arg Glu Gly Val Met Glu Phe Leu Leu Ala Asn His Pro Leu Asp Cys

115 120 125

Pro Ile Cys Asp Gln Gly Gly Glu Cys Asp Leu Gln Asp Gln Ser Met

130 135 140

Met Phe Gly Asn Asp Arg Ser Arg Phe Leu Glu Gly Lys Arg Ala Val

145 150 155 160

Glu Asp Lys Asn Ile Gly Pro Leu Val Lys Thr Ile Met Thr Arg Cys

165 170 175

Ile Gln Cys Thr Arg Cys Ile Arg Phe Ala Ser Glu Ile Ala Gly Val

180 185 190

Asp Asp Leu Gly Thr Thr Gly Arg Gly Asn Asp Met Gln Val Gly Thr

195 200 205

Tyr Ile Glu Lys Met Phe Met Ser Glu Leu Ser Gly Asn Ile Ile Asp

210 215 220

Ile Cys Pro Val Gly Ala Leu Thr Ser Lys Pro Tyr Ala Phe Thr Ala

225 230 235 240

Arg Pro Trp Glu Thr Arg Lys Thr Glu Ser Ile Asp Val Met Asp Ala

245 250 255

Val Gly Ser Asn Ile Val Val Ser Thr Arg Thr Gly Glu Val Met Arg

260 265 270

Ile Leu Pro Arg Met His Glu Asp Ile Asn Glu Glu Trp Ile Ser Asp

275 280 285

Lys Thr Arg Phe Ala Tyr Asp Gly Leu Lys Arg Gln Arg Leu Thr Glu

290 295 300

Pro Met Val Arg Asn Glu Lys Gly Leu Leu Thr Tyr Thr Ser Trp Glu

305 310 315 320

Asp Ala Leu Ser Arg Val Ala Gly Met Leu Gln Ser Phe Gln Gly Lys

325 330 335

Asp Val Ala Ala Ile Ala Gly Gly Leu Val Asp Ala Glu Ala Leu Val

340 345 350

Ala Leu Lys Asp Leu Leu Asn Arg Val Asp Ser Asp Thr Leu Cys Thr

355 360 365

Glu Glu Val Phe Pro Thr Ala Gly Ala Gly Thr Asp Leu Arg Ser Asn

370 375 380

Tyr Leu Leu Asn Thr Thr Ile Ala Gly Val Glu Glu Ala Asp Val Val

385 390 395 400

Leu Leu Val Gly Thr Asn Pro Arg Phe Glu Ala Pro Leu Phe Asn Ala

405 410 415

Trp Ile Arg Lys Ser Trp Leu His Asn Asp Leu Lys Val Ala Leu Ile

420 425 430

Gly Ser Pro Val Asp Leu Thr Tyr Thr Tyr Asp His Leu Gly Asp Ser

435 440 445

Pro Lys Ile Leu Gln Asp Ile Ala Ser Gly Ser His Pro Phe Ser Gln

450 455 460

Val Leu Lys Glu Ala Lys Lys Pro Met Val Val Leu Gly Ser Ser Ala

465 470 475 480

Leu Gln Arg Asn Asp Gly Ala Ala Ile Leu Ala Ala Val Ser Ser Ile

485 490 495

Ala Gln Lys Ile Arg Met Thr Ser Gly Val Thr Gly Asp Trp Lys Val

500 505 510

Met Asn Ile Leu His Arg Ile Ala Ser Gln Val Ala Ala Leu Asp Leu

515 520 525

Gly Tyr Lys Pro Gly Val Glu Ala Ile Arg Lys Asn Pro Pro Lys Val

530 535 540

Leu Phe Leu Leu Gly Ala Asp Gly Gly Cys Ile Thr Arg Gln Asp Leu

545 550 555 560

Pro Lys Asp Cys Phe Ile Ile Tyr Gln Gly His His Gly Asp Val Gly

565 570 575

Ala Pro Ile Ala Asp Val Ile Leu Pro Gly Ala Ala Tyr Thr Glu Lys

580 585 590

Ser Ala Thr Tyr Val Asn Thr Glu Gly Arg Ala Gln Gln Thr Lys Val

595 600 605

Ala Val Thr Pro Pro Gly Leu Ala Arg Glu Asp Trp Lys Ile Ile Arg

610 615 620

Ala Leu Ser Glu Ile Ala Gly Met Thr Leu Pro Tyr Asp Thr Leu Asp

625 630 635 640

Gln Val Arg Asn Arg Leu Glu Glu Phe Ser Pro Asn Leu Val Arg Tyr

645 650 655

Asp Asp Ile Glu Gly Ala Asn Tyr Phe Gln Gln Ala Asn Glu Leu Ser

660 665 670

Lys Leu Val Asn Gln Gln Leu Leu Ala Asp Pro Leu Val Pro Pro Gln

675 680 685

Leu Thr Leu Lys Asp Phe Tyr Met Thr Asp Ser Ile Ser Arg Ala Ser

690 695 700

Gln Thr Met Ala Lys Cys Val Lys Ala Val Thr Glu Gly Ala Gln Ala

705 710 715 720

Val Glu Glu Pro Ser Ile Cys

725

<210> 43

<211> 491

<212> PRT

<213> Homo sapiens

<220>

<221> Pre-B cell enhancing factor precursor

<222> (1)..(491)

<223> swissprot accession No. as of 09 Dec 2002: P43490

<400> 43

Met Asn Pro Ala Ala Glu Ala Glu Phe Asn Ile Leu Leu Ala Thr Asp
1 5 10 15

Ser Tyr Lys Val Thr His Tyr Lys Gln Tyr Pro Pro Asn Thr Ser Lys
20 25 30

Val Tyr Ser Tyr Phe Glu Cys Arg Glu Lys Lys Thr Glu Asn Ser Lys
35 40 45

Leu Arg Lys Val Lys Tyr Glu Glu Thr Val Phe Tyr Gly Leu Gln Tyr
50 55 60

Ile Leu Asn Lys Tyr Leu Lys Gly Lys Val Val Thr Lys Glu Lys Ile
65 70 75 80

Gln Glu Ala Lys Asp Val Tyr Lys Glu His Phe Gln Asp Asp Val Phe
85 90 95

Asn Glu Lys Gly Trp Asn Tyr Ile Leu Glu Lys Tyr Asp Gly His Leu
100 105 110

Pro Ile Glu Ile Lys Ala Val Pro Glu Gly Phe Val Ile Pro Arg Gly
115 120 125

Asn Val Leu Phe Thr Val Glu Asn Thr Asp Pro Glu Cys Tyr Trp Leu
130 135 140

Thr Asn Trp Ile Glu Thr Ile Leu Val Gln Ser Trp Tyr Pro Ile Thr
145 150 155 160

Val Ala Thr Asn Ser Arg Glu Gln Lys Lys Ile Leu Ala Lys Tyr Leu
165 170 175

Leu Glu Thr Ser Gly Asn Leu Asp Gly Leu Glu Tyr Lys Leu His Asp
180 185 190

Phe Gly Tyr Arg Gly Val Ser Ser Gln Glu Thr Ala Gly Ile Gly Ala
195 200 205

Ser Ala His Leu Val Asn Phe Lys Gly Thr Asp Thr Val Ala Gly Leu
210 215 220

Ala Leu Ile Lys Lys Tyr Tyr Gly Thr Lys Asp Pro Val Pro Gly Tyr
225 230 235 240

Ser Val Pro Ala Ala Glu His Ser Thr Ile Thr Ala Trp Gly Lys Asp
245 250 255

His Glu Lys Asp Ala Phe Glu His Ile Val Thr Gln Phe Ser Ser Val
260 265 270

Pro Val Ser Val Val Ser Asp Ser Tyr Asp Ile Tyr Asn Ala Cys Glu
275 280 285

Lys Ile Trp Gly Glu Asp Leu Arg His Leu Ile Val Ser Arg Ser Thr
290 295 300

Gln Ala Pro Leu Ile Ile Arg Pro Asp Ser Gly Asn Pro Leu Asp Thr
305 310 315 320

Val Leu Lys Val Leu Glu Ile Leu Gly Lys Lys Phe Pro Val Thr Glu
325 330 335
Asn Ser Lys Gly Tyr Lys Leu Leu Pro Pro Tyr Leu Arg Val Ile Gln
340 345 350
Gly Asp Gly Val Asp Ile Asn Thr Leu Gln Glu Ile Val Glu Gly Met
355 360 365
Lys Gln Lys Met Trp Ser Ile Glu Asn Ile Ala Phe Gly Ser Gly Gly
370 375 380
Gly Leu Leu Gln Lys Leu Thr Arg Asp Leu Leu Asn Cys Ser Phe Lys
385 390 395 400
Cys Ser Tyr Val Val Thr Asn Gly Leu Gly Ile Asn Val Phe Lys Asp
405 410 415
Pro Val Ala Asp Pro Asn Lys Arg Ser Lys Lys Gly Arg Leu Ser Leu
420 425 430
His Arg Thr Pro Ala Gly Asn Phe Val Thr Leu Glu Glu Gly Lys Gly
435 440 445
Asp Leu Glu Glu Tyr Gly Gln Asp Leu Leu His Thr Val Phe Lys Asn
450 455 460
Gly Lys Val Thr Lys Ser Tyr Ser Phe Asp Glu Ile Arg Lys Asn Ala
465 470 475 480
Gln Leu Asn Ile Glu Leu Glu Ala Ala His His
485 490

<210> 44

<211> 135

<212> PRT

<213> Homo sapiens

<220>

<221> Retinol-binding protein I, cellular

<222> (1)..(135)

<223> swissprot accession No. as of 09 Dec 2002: P09455

<400> 44

Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
1 5 10 15

Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
20 25 30

Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
35 40 45

His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
50 55 60

Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
65 70 75 80

Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
85 90 95

Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
100 105 110

Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
115 120 125

Gln Val Phe Lys Lys Val Gln
130 135

<210> 45

<211> 544

<212> PRT

<213> Homo sapiens

<220>

<221> T-complex protein 1, gamma subunit

<222> (1)..(544)

<223> swissprot accession No. as of 09 Dec 2002: P49368

<400> 45

Met Gly His Arg Pro Val Leu Val Leu Ser Gln Asn Thr Lys Arg Glu
1 5 10 15

Ser Gly Arg Lys Val Gln Ser Gly Asn Ile Asn Ala Ala Lys Thr Ile
20 25 30

Ala Asp Ile Ile Arg Thr Cys Leu Gly Pro Lys Ser Met Met Lys Met
35 40 45

Leu Leu Asp Pro Met Gly Gly Ile Val Met Thr Asn Asp Gly Asn Ala
50 55 60

Ile Leu Arg Glu Ile Gln Val Gln His Pro Ala Ala Lys Ser Met Ile
65 70 75 80

Glu Ile Ser Arg Thr Gln Asp Glu Glu Val Gly Asp Gly Thr Thr Ser
85 90 95

Val Ile Ile Leu Ala Gly Glu Met Leu Ser Val Ala Glu His Phe Leu

100 105 110

Glu Gln Gln Met His Pro Thr Val Val Ile Ser Ala Tyr Arg Lys Ala

115 120 125

Leu Asp Asp Met Ile Ser Thr Leu Lys Lys Ile Ser Ile Pro Val Asp

130 135 140

Ile Ser Asp Ser Asp Met Met Leu Asn Ile Ile Asn Ser Ser Ile Thr

145 150 155 160

Thr Lys Ala Ile Ser Arg Trp Ser Ser Leu Ala Cys Asn Ile Ala Leu

165 170 175

Asp Ala Val Lys Met Val Gln Phe Glu Glu Asn Gly Arg Lys Glu Ile

180 185 190

Asp Ile Lys Lys Tyr Ala Arg Val Glu Lys Ile Pro Gly Gly Ile Ile

195 200 205

Glu Asp Ser Cys Val Leu Arg Gly Val Met Ile Asn Lys Asp Val Thr

210 215 220

His Pro Arg Met Arg Arg Tyr Ile Lys Asn Pro Arg Ile Val Leu Leu

225 230 235 240

Asp Ser Ser Leu Glu Tyr Lys Lys Gly Glu Ser Gln Thr Asp Ile Glu

245 250 255

Ile Thr Arg Glu Glu Asp Phe Thr Arg Ile Leu Gln Met Glu Glu Glu

260 265 270

Tyr Ile Gln Gln Leu Cys Glu Asp Ile Ile Gln Leu Lys Pro Asp Val

275 280 285

Val Ile Thr Glu Lys Gly Ile Ser Asp Leu Ala Gln His Tyr Leu Met

290 295 300

Arg Ala Asn Ile Thr Ala Ile Arg Arg Val Arg Lys Thr Asp Asn Asn

305 310 315 320

Arg Ile Ala Arg Ala Cys Gly Ala Arg Ile Val Ser Arg Pro Glu Glu

325 330 335

Leu Arg Glu Asp Asp Val Gly Thr Gly Ala Gly Leu Leu Glu Ile Lys

340 345 350

Lys Ile Gly Asp Glu Tyr Phe Thr Phe Ile Thr Asp Cys Lys Asp Pro

355 360 365

Lys Ala Cys Thr Ile Leu Leu Arg Gly Ala Ser Lys Glu Ile Leu Ser

370 375 380

Glu Val Glu Arg Asn Leu Gln Asp Ala Met Gln Val Cys Arg Asn Val

385 390 395 400

Leu Leu Asp Pro Gln Leu Val Pro Gly Gly Gly Ala Ser Glu Met Ala

405 410 415

Val Ala His Ala Leu Thr Glu Lys Ser Lys Ala Met Thr Gly Val Glu

420 425 430

Gln Trp Pro Tyr Arg Ala Val Ala Gln Ala Leu Glu Val Ile Pro Arg

435 440 445

Thr Leu Ile Gln Asn Cys Gly Ala Ser Thr Ile Arg Leu Leu Thr Ser

450 455 460

Leu Arg Ala Lys His Thr Gln Glu Asn Cys Glu Thr Trp Gly Val Asn

465 470 475 480

Gly Glu Thr Gly Thr Leu Val Asp Met Lys Glu Leu Gly Ile Trp Glu

485 490 495

Pro Leu Ala Val Lys Leu Gln Thr Tyr Lys Thr Ala Val Glu Thr Ala

500 505 510

Val Leu Leu Leu Arg Ile Asp Asp Ile Val Ser Gly His Lys Lys Lys

515 520 525

Gly Asp Asp Gln Ser Arg Gln Gly Gly Ala Pro Asp Ala Gly Gln Glu

530 535 540

<210> 46

<211> 461

<212> PRT

<213> Homo sapiens

<220>

<221> Placental ribonuclease inhibitor

<222> (1)..(461)

<223> swissprot accession No. as of 09 Dec 2002: P13489

<400> 46

Met Ser Leu Asp Ile Gln Ser Leu Asp Ile Gln Cys Glu Glu Leu Ser

1 5 10 15

Asp Ala Arg Trp Ala Glu Leu Leu Pro Leu Leu Gln Gln Cys Gln Val

20 25 30

Val Arg Leu Asp Asp Cys Gly Leu Thr Glu Ala Arg Cys Lys Asp Ile

35 40 45

Ser Ser Ala Leu Arg Val Asn Pro Ala Leu Ala Glu Leu Asn Leu Arg

50 55 60

Ser Asn Glu Leu Gly Asp Val Gly Val His Cys Val Leu Gln Gly Leu

65 70 75 80

Gln Thr Pro Ser Cys Lys Ile Gln Lys Leu Ser Leu Gln Asn Cys Cys
85 90 95
Leu Thr Gly Ala Gly Cys Gly Val Leu Ser Ser Thr Leu Arg Thr Leu
100 105 110
Pro Thr Leu Gln Glu Leu His Leu Ser Asp Asn Leu Leu Gly Asp Ala
115 120 125
Gly Leu Gln Leu Leu Cys Glu Gly Leu Leu Asp Pro Gln Cys Arg Leu
130 135 140
Glu Lys Leu Gln Leu Glu Tyr Cys Ser Leu Ser Ala Ala Ser Cys Glu
145 150 155 160
Pro Leu Ala Ser Val Leu Arg Ala Lys Pro Asp Phe Lys Glu Leu Thr
165 170 175
Val Ser Asn Asn Asp Ile Asn Glu Ala Gly Val Arg Val Leu Cys Gln
180 185 190
Gly Leu Lys Asp Ser Pro Cys Gln Leu Glu Ala Leu Lys Leu Glu Ser
195 200 205
Cys Gly Val Thr Ser Asp Asn Cys Arg Asp Leu Cys Gly Ile Val Ala
210 215 220
Ser Lys Ala Ser Leu Arg Glu Leu Ala Leu Gly Ser Asn Lys Leu Gly
225 230 235 240
Asp Val Gly Met Ala Glu Leu Cys Pro Gly Leu Leu His Pro Ser Ser
245 250 255
Arg Leu Arg Thr Leu Trp Ile Trp Glu Cys Gly Ile Thr Ala Lys Gly
260 265 270
Cys Gly Asp Leu Cys Arg Val Leu Arg Ala Lys Glu Ser Leu Lys Glu
275 280 285

Leu Ser Leu Ala Gly Asn Glu Leu Gly Asp Glu Gly Ala Arg Leu Leu
290 295 300

Cys Glu Thr Leu Leu Glu Pro Gly Cys Gln Leu Glu Ser Leu Trp Val
305 310 315 320

Lys Ser Cys Ser Phe Thr Ala Ala Cys Cys Ser His Phe Ser Ser Val
325 330 335

Leu Ala Gln Asn Arg Phe Leu Leu Glu Leu Gln Ile Ser Asn Asn Arg
340 345 350

Leu Glu Asp Ala Gly Val Arg Glu Leu Cys Gln Gly Leu Gly Gln Pro
355 360 365

Gly Ser Val Leu Arg Val Leu Trp Leu Ala Asp Cys Asp Val Ser Asp
370 375 380

Ser Ser Cys Ser Ser Leu Ala Ala Thr Leu Leu Ala Asn His Ser Leu
385 390 395 400

Arg Glu Leu Asp Leu Ser Asn Asn Cys Leu Gly Asp Ala Gly Ile Leu
405 410 415

Gln Leu Val Glu Ser Val Arg Gln Pro Gly Cys Leu Leu Glu Gln Leu
420 425 430

Val Leu Tyr Asp Ile Tyr Trp Ser Glu Glu Met Glu Asp Arg Leu Gln
435 440 445

Ala Leu Glu Lys Asp Lys Pro Ser Leu Arg Val Ile Ser
450 455 460

<210> 47

<211> 317

<212> PRT

<213> Homo sapiens

<220>

<221> Guanine nucleotide-binding protein beta subunit-like protein 12.3

<222> (1)..(317)

<223> swissprot accession No. as of 09 Dec 2002: P25388

<400> 47

```
Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
1               5                  10                  15
Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
            20                  25                  30
Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
        35                  40                  45
Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
    50                  55                  60
Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
65                  70                  75                  80
Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
                85                  90                  95
Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
            100                 105                 110
Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
        115                 120                 125
Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
    130                 135                 140
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Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
145 150 155 160
Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
165 170 175
Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
180 185 190
Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
195 200 205
Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
210 215 220
Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
225 230 235 240
Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
245 250 255
Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
260 265 270
Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
275 280 285
Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
290 295 300
Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
305 310 315

<210> 48

<211> 172

<212> PRT

<213> Homo sapiens

<220>

<221> Myosin regulatory light chain 2

<222> (1)..(172)

<223> swissprot accession No. as of 10 Dec 2002: P24844

<400> 48

Met Ser Ser Lys Arg Ala Lys Ala Lys Thr Thr Lys Lys Arg Pro Gln
1 5 10 15

Arg Ala Thr Ser Asn Val Phe Ala Met Phe Asp Gln Ser Gln Ile Gln
20 25 30

Glu Phe Lys Glu Ala Phe Asn Met Ile Asp Gln Asn Arg Asp Gly Phe
35 40 45

Ile Asp Lys Glu Asp Leu His Asp Met Leu Ala Ser Leu Gly Lys Asn
50 55 60

Pro Thr Asp Glu Tyr Leu Glu Gly Met Met Ser Glu Ala Pro Gly Pro
65 70 75 80

Ile Asn Phe Thr Met Phe Leu Thr Met Phe Gly Glu Lys Leu Asn Gly
85 90 95

Thr Asp Pro Glu Asp Val Ile Arg Asn Ala Phe Ala Cys Phe Asp Glu
100 105 110

Glu Ala Ser Gly Phe Ile His Glu Asp His Leu Arg Glu Leu Leu Thr
115 120 125

Thr Met Gly Asp Arg Phe Thr Asp Glu Glu Val Asp Glu Met Tyr Arg

130 135 140

Glu Ala Pro Ile Asp Lys Lys Gly Asn Phe Asn Tyr Val Glu Phe Thr

145 150 155 160

Arg Ile Leu Lys His Gly Ala Lys Asp Lys Asp Asp

165 170

<210> 49

<211> 114

<212> PRT

<213> Homo sapiens

<220>

<221> Calgranulin B

<222> (1)..(114)

<223> swissprot accession No. as of 10 Dec 2002: P06702

<400> 49

Met Thr Cys Lys Met Ser Gln Leu Glu Arg Asn Ile Glu Thr Ile Ile

1 5 10 15

Asn Thr Phe His Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu

20 25 30

Asn Gln Gly Glu Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe

35 40 45

Leu Lys Lys Glu Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu

50 55 60

Asp Leu Asp Thr Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile
65 70 75 80
Met Leu Met Ala Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu
85 90 95
Gly Asp Glu Gly Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly
100 105 110
Thr Pro

<210> 50
<211> 348
<212> PRT
<213> Homo sapiens
<220>
<221> Macrophage capping protein
<222> (1)..(348)
<223> swissprot accession No. as of 10 Dec 2002: P40121

<400> 50

Met Tyr Thr Ala Ile Pro Gln Ser Gly Ser Pro Phe Pro Gly Ser Val
1 5 10 15
Gln Asp Pro Gly Leu His Val Trp Arg Val Glu Lys Leu Lys Pro Val
20 25 30
Pro Val Ala Gln Glu Asn Gln Gly Val Phe Phe Ser Gly Asp Ser Tyr

35 40 45

Leu Val Leu His Asn Gly Pro Glu Glu Val Ser His Leu His Leu Trp

50 55 60

Ile Gly Gln Gln Ser Ser Arg Asp Glu Gln Gly Ala Cys Ala Val Leu

65 70 75 80

Ala Val His Leu Asn Thr Leu Leu Gly Glu Arg Pro Val Gln His Arg

85 90 95

Glu Val Gln Gly Asn Glu Ser Asp Leu Phe Met Ser Tyr Phe Pro Arg

100 105 110

Gly Leu Lys Tyr Gln Glu Gly Gly Val Glu Ser Ala Phe His Lys Thr

115 120 125

Ser Thr Gly Ala Pro Ala Ala Ile Lys Lys Leu Tyr Gln Val Lys Gly

130 135 140

Lys Lys Asn Ile Arg Ala Thr Glu Arg Ala Leu Asn Trp Asp Ser Phe

145 150 155 160

Asn Thr Gly Asp Cys Phe Ile Leu Asp Leu Gly Gln Asn Ile Phe Ala

165 170 175

Trp Cys Gly Gly Lys Ser Asn Ile Leu Glu Arg Asn Lys Ala Arg Asp

180 185 190

Leu Ala Leu Ala Ile Arg Asp Ser Glu Arg Gln Gly Lys Ala Gln Val

195 200 205

Glu Ile Val Thr Asp Gly Glu Glu Pro Ala Glu Met Ile Gln Val Leu

210 215 220

Gly Pro Lys Pro Ala Leu Lys Glu Gly Asn Pro Glu Glu Asp Leu Thr

225 230 235 240

Ala Asp Lys Ala Asn Ala Gln Ala Ala Ala Leu Tyr Lys Val Ser Asp

245 250 255

Ala Thr Gly Gln Met Asn Leu Thr Lys Val Ala Asp Ser Ser Pro Phe

260 265 270

Ala Leu Glu Leu Leu Ile Ser Asp Asp Cys Phe Val Leu Asp Asn Gly

275 280 285

Leu Cys Gly Lys Ile Tyr Ile Trp Lys Gly Arg Lys Ala Asn Glu Lys

290 295 300

Glu Arg Gln Ala Ala Leu Gln Val Ala Glu Gly Phe Ile Ser Arg Met

305 310 315 320

Gln Tyr Ala Pro Asn Thr Gln Val Glu Ile Leu Pro Gln Gly Arg Glu

325 330 335

Ser Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Lys

340 345

<210> 51

<211> 346

<212> PRT

<213> Homo sapiens

<220>

<221> Annexin I

<222> (1)..(346)

<223> swissprot accession No. as of 10 Dec 2002: P04083

<400> 51

Met Ala Met Val Ser Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn
1 5 10 15
Glu Glu Gln Glu Tyr Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro
20 25 30
Gly Ser Ala Val Ser Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val
35 40 45
Ala Ala Leu His Lys Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr
50 55 60
Ile Ile Asp Ile Leu Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile
65 70 75 80
Lys Ala Ala Tyr Leu Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu
85 90 95
Lys Lys Ala Leu Thr Gly His Leu Glu Glu Val Val Leu Ala Leu Leu
100 105 110
Lys Thr Pro Ala Gln Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys
115 120 125
Gly Leu Gly Thr Asp Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg
130 135 140
Thr Asn Lys Glu Ile Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu
145 150 155 160
Lys Arg Asp Leu Ala Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe
165 170 175
Arg Asn Ala Leu Leu Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe
180 185 190
Gly Val Asn Glu Asp Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu
195 200 205

Ala Gly Glu Arg Arg Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile
210 215 220
Leu Thr Thr Arg Ser Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr
225 230 235 240
Thr Lys Tyr Ser Lys His Asp Met Asn Lys Val Leu Asp Leu Glu Leu
245 250 255
Lys Gly Asp Ile Glu Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr
260 265 270
Ser Lys Pro Ala Phe Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly
275 280 285
Val Gly Thr Arg His Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser
290 295 300
Glu Ile Asp Met Asn Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly
305 310 315 320
Ile Ser Leu Cys Gln Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu
325 330 335
Lys Ile Leu Val Ala Leu Cys Gly Gly Asn
340 345

<210> 52
<211> 469
<212> PRT
<213> Homo sapiens
<220>
<221> Keratin, type II cytoskeletal 7

<222> (1)..(469)

<223> swissprot accession No. as of 10 Dec 2002: P08729

<400> 52

Met Ser Ile His Phe Ser Ser Pro Val Phe Thr Ser Arg Ser Ala Ala
1 5 10 15

Phe Ser Gly Arg Gly Ala Gln Val Arg Leu Ser Ser Ala Arg Pro Gly
20 25 30

Gly Leu Gly Ser Ser Ser Leu Tyr Gly Leu Gly Ala Ser Arg Pro Arg
35 40 45

Val Ala Val Arg Ser Ala Tyr Gly Gly Pro Val Gly Ala Gly Ile Arg
50 55 60

Glu Val Thr Ile Asn Gln Ser Leu Leu Ala Pro Leu Arg Leu Asp Ala
65 70 75 80

Asp Pro Ser Leu Gln Arg Val Arg Gln Glu Glu Ser Glu Gln Ile Lys
85 90 95

Thr Leu Asn Asn Lys Phe Ala Ser Phe Ile Asp Lys Val Arg Phe Leu
100 105 110

Glu Gln Gln Asn Lys Leu Leu Glu Thr Lys Trp Thr Leu Leu Gln Glu
115 120 125

Gln Lys Ser Ala Lys Ser Ser Arg Leu Pro Asp Ile Phe Glu Ala Gln
130 135 140

Ile Ala Gly Leu Arg Gly Gln Leu Glu Ala Leu Gln Val Asp Gly Gly
145 150 155 160

Arg Leu Glu Gln Gly Leu Arg Thr Met Gln Asp Val Val Glu Asp Phe

165 170 175

Lys Asn Lys Tyr Glu Asp Glu Ile Asn Arg Arg Thr Ala Ala Glu Asn

180 185 190

Glu Phe Val Val Leu Lys Lys Asp Val Asp Ala Ala Tyr Met Ser Lys

195 200 205

Val Glu Leu Glu Ala Lys Val Asp Ala Leu Asn Asp Glu Ile Asn Phe

210 215 220

Leu Arg Thr Leu Asn Glu Thr Glu Leu Thr Glu Leu Gln Ser Gln Ile

225 230 235 240

Ser Asp Thr Ser Val Val Leu Ser Met Asp Asn Ser Arg Ser Leu Asp

245 250 255

Leu Asp Gly Ile Ile Ala Glu Val Lys Ala Gln Tyr Glu Glu Met Ala

260 265 270

Lys Cys Ser Arg Ala Glu Ala Glu Ala Trp Tyr Gln Thr Lys Phe Glu

275 280 285

Thr Leu Gln Ala Gln Ala Gly Lys His Gly Asp Asp Leu Arg Asn Thr

290 295 300

Arg Asn Glu Ile Ser Glu Met Asn Arg Ala Ile Gln Arg Leu Gln Ala

305 310 315 320

Glu Ile Asp Asn Ile Lys Asn Gln Arg Ala Lys Leu Glu Ala Ala Ile

325 330 335

Ala Glu Ala Glu Glu Arg Gly Glu Leu Ala Leu Lys Asp Ala Arg Ala

340 345 350

Lys Gln Glu Glu Leu Glu Ala Ala Leu Gln Arg Ala Lys Gln Asp Met

355 360 365

Ala Arg Gln Leu Arg Glu Tyr Gln Glu Leu Met Ser Val Lys Leu Ala

370 375 380

Leu Asp Ile Glu Ile Ala Thr Tyr Arg Lys Leu Leu Glu Gly Glu Glu

385 390 395 400

Ser Arg Leu Ala Gly Asp Gly Val Gly Ala Val Asn Ile Ser Val Met

405 410 415

Asn Ser Thr Gly Gly Ser Ser Ser Gly Gly Gly Ile Gly Leu Thr Leu

420 425 430

Gly Gly Thr Met Gly Ser Asn Ala Leu Ser Phe Ser Ser Ser Ala Gly

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Pro Gly Leu Leu Lys Ala Tyr Ser Ile Arg Thr Ala Ser Ala Ser Arg

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Arg Ser Ala Arg Asp

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<211> 836

<212> PRT

<213> Homo sapiens

<220>

<221> Osteoblast specific factor 2 precursor

<222> (1)..(836)

<223> trEMBL accession No. as of 10 Dec 2002: Q15063

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Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35 40 45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50 55 60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65 70 75 80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85 90 95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100 105 110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115 120 125
Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
130 135 140
Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
145 150 155 160
Leu Leu Asn Ala Leu His Ser His Met Ile Asn Lys Arg Met Leu Thr
165 170 175
Lys Asp Leu Lys Asn Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu
180 185 190
Gly Leu Phe Ile Asn His Tyr Pro Asn Gly Val Val Thr Val Asn Cys

195 200 205

Ala Arg Ile Ile His Gly Asn Gln Ile Ala Thr Asn Gly Val Val His

210 215 220

Val Ile Asp Arg Val Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe

225 230 235 240

Ile Glu Ala Glu Asp Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr

245 250 255

Ser Asp Ile Leu Glu Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe

260 265 270

Ala Pro Thr Asn Glu Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu

275 280 285

Arg Phe Met Gly Asp Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His

290 295 300

Ile Leu Asn Thr Leu Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val

305 310 315 320

Phe Glu Thr Leu Glu Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp

325 330 335

Ser Ile Thr Val Asn Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val

340 345 350

Thr Asn Asn Gly Val Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp

355 360 365

Ser Ala Lys Gln Val Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe

370 375 380

Thr Asp Leu Val Ala Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp

385 390 395 400

Gly Glu Tyr Thr Leu Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp

405 410 415

Thr Leu Ser Met Val Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His

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Ile Leu Lys Val Lys Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile

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Leu Glu Thr Ile Gly Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr

450 455 460

Ala Val Cys Ile Glu Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly

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Arg Asn Gly Ala Ile His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu

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Lys Ser Leu His Glu Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe

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Leu Ser Leu Leu Glu Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro

515 520 525

Gly Asp Trp Thr Leu Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met

530 535 540

Thr Ser Glu Glu Lys Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln

545 550 555 560

Asn Ile Ile Leu Tyr His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly

565 570 575

Phe Glu Pro Gly Val Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys

580 585 590

Ile Phe Leu Lys Glu Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys

595 600 605

Ser Lys Glu Ser Asp Ile Met Thr Thr Asn Gly Val Ile His Val Val

610 615 620

Asp Lys Leu Leu Tyr Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu

625 630 635 640

Leu Glu Ile Leu Asn Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val

645 650 655

Arg Gly Ser Thr Phe Lys Glu Ile Pro Val Thr Val Tyr Thr Thr Lys

660 665 670

Ile Ile Thr Lys Val Val Glu Pro Lys Ile Lys Val Ile Glu Gly Ser

675 680 685

Leu Gln Pro Ile Ile Lys Thr Glu Gly Pro Thr Leu Thr Lys Val Lys

690 695 700

Ile Glu Gly Glu Pro Glu Phe Arg Leu Ile Lys Glu Gly Glu Thr Ile

705 710 715 720

Thr Glu Val Ile His Gly Glu Pro Ile Ile Lys Lys Tyr Thr Lys Ile

725 730 735

Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg Glu Glu

740 745 750

Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser Thr Gly

755 760 765

Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu Glu Val

770 775 780

Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu Phe Glu

785 790 795 800

Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val Arg Lys

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Gly Arg Ser Gln

835

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<213> Homo sapiens

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<222> (1)..(687)

<223> swissprot accession No. P21980

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35 40 45

Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
50 55 60

Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
65 70 75 80

Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
85 90 95

Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
100 105 110

Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
115 120 125

Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
130 135 140

Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
145 150 155 160

Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
165 170 175

Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
180 185 190

Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
195 200 205

Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
210 215 220

Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225 230 235 240

Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
245 250 255

Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
260 265 270

Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
275 280 285

Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
290 295 300
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
305 310 315 320
Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
325 330 335
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
340 345 350
Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
355 360 365
Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
370 375 380
Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
385 390 395 400
Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
405 410 415
Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
420 425 430
Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
435 440 445
Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
450 455 460
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465 470 475 480
Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
485 490 495

Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg
500 505 510

Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
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530 535 540

Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
545 550 555 560

Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
565 570 575

Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
580 585 590

Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
595 600 605

Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
610 615 620

Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
625 630 635 640

Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro
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Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala
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<211> 204

<212> PRT

<213> Homo sapiens

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<221> Rho GDP-dissociation inhibitor 1

<222> (1)..(204)

<223> swissprot accession No. as of 10 Dec 2002: P52565

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35 40 45
Arg Lys Tyr Lys Glu Ala Leu Leu Gly Arg Val Ala Val Ser Ala Asp
50 55 60
Pro Asn Val Pro Asn Val Val Val Thr Gly Leu Thr Leu Val Cys Ser
65 70 75 80
Ser Ala Pro Gly Pro Leu Glu Leu Asp Leu Thr Gly Asp Leu Glu Ser
85 90 95
Phe Lys Lys Gln Ser Phe Val Leu Lys Glu Gly Val Glu Tyr Arg Ile
100 105 110
Lys Ile Ser Phe Arg Val Asn Arg Glu Ile Val Ser Gly Met Lys Tyr

115 120 125

Ile Gln His Thr Tyr Arg Lys Gly Val Lys Ile Asp Lys Thr Asp Tyr

130 135 140

Met Val Gly Ser Tyr Gly Pro Arg Ala Glu Glu Tyr Glu Phe Leu Thr

145 150 155 160

Pro Val Glu Glu Ala Pro Lys Gly Met Leu Ala Arg Gly Ser Tyr Ser

165 170 175

Ile Lys Ser Arg Phe Thr Asp Asp Asp Lys Thr Asp His Leu Ser Trp

180 185 190

Glu Trp Asn Leu Thr Ile Lys Lys Asp Trp Lys Asp

195 200

Claims

1. A marker for diagnosis of pancreatic cancer comprising at least one polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3.

2. The marker of claim 1 wherein the group from which at least one polypeptide is selected consists of the polypeptides listed in table 2.

3. A polypeptide selected from the group consisting of the polypeptides listed in tables 2 and 3, for use as a marker or as a component of a marker for diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer.

4. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of a marker of claims 1 or 2.

5. The in vitro method of claim 4, wherein the marker comprises at least two polypeptides.

6. The in vitro method of claims 4 or 5 wherein said biological sample is derived from the group consisting of serum, plasma, pancreatic juice and cells of pancreatic tissue.

7. An in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of

a) obtaining a biological sample; and

b) detecting and/or measuring the increase of at least one nucleic acid coding for the marker of claims 1 or 2.

8. The in vitro method of claim 7, wherein said nucleic acid molecule is RNA or DNA.

9. The in vitro method of claim 8, wherein said DNA is a cDNA.

10. The in vitro method of any one of claims 7 to 9, wherein the expression levels of at least one of said nucleic acids in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same nucleic acids in a healthy individual.

11. The in vitro method of any one of claims 4 to 6, wherein the expression level of said marker in an individual suspected to suffer from pancreatic cancer and/or to be susceptible to pancreatic cancer is compared to the expression levels of the same marker in a healthy individual.

12. The in vitro method of claim 11, wherein an increase of the expression levels of said marker is indicative of pancreatic cancer or the susceptibility to pancreatic cancer.

13. A screening method for identifying and/or obtaining a compound which interacts with a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting said polypeptide with a compound or a plurality of compounds under conditions which allow interaction of said compound with said polypeptide; and

b) detecting the interaction between said compound or plurality of compounds with said polypeptide.

14. A screening method for identifying and/or obtaining a compound which is an inhibitor or an antagonist of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a said polypeptide with a compound identified and/or obtained by the screening method of claim 13 under conditions which allow interaction of said compound with said polypeptide;

b) determining the activity of said polypeptide;

c) determining the activity of said polypeptide expressed in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the activity as determined in (b) and (c), wherein a decreased activity determined in (b) in comparison to (c) is indicative for an inhibitor or antagonist.

15. A screening method for identifying and/or obtaining a compound which is an inhibitor of the expression of a polypeptide listed in tables 2 and/or 3 whose expression is upregulated in pancreatic cancer, comprising the steps of

a) contacting a host which expresses said polypeptide with a compound,

b) determining the expression level and/or activity of said polypeptide;

c) determining the expression level and/or activity of said polypeptide in the host as defined in (a), which has not been contacted with said compound; and

d) quantitatively relating the expression level of said polypeptide as determined in (b) and (c), wherein a decreased expression level determined in (b) in comparison to (c) is indicative for an inhibitor of the expression of said polypeptide.

16. A compound identified and/or obtained by the screening methods of any one of claims 13 to 15.

17. A pharmaceutical composition comprising the compound of claim 16.

18. A method for the preparation of the pharmaceutical composition of claim 17 comprising formulating the compound of claim 16 in a pharmaceutically acceptable carrier or diluent.

19. Use of a compound of claim 16 for the preparation of a medicament for the treatment or prevention of pancreatic cancer.

20. Use of a compound of claim 16 for the preparation of a diagnostic composition for diagnosing pancreatic cancer or a predisposition for pancreatic cancer.

21. The use of claim 19 or 20 wherein said compound comprises an antibody, an antibody-derivative, an antibody fragment, a peptide or an antisense construct.

22. Antibodies against the proteins listed in tables 2 and/or 3, or antigen-binding fragments thereof, for the use in an in vitro method for the diagnosis of pancreatic cancer.

23. A kit for the diagnosis of pancreatic cancer comprising one or more of the antibodies, or antigen-binding fragments thereof, of claim 22.

24. A kit for the diagnosis of pancreatic cancer comprising one or more of the nucleic acids coding for the marker of claims 1 or 2.

25. A kit for screening of compounds that activate or inhibit any of the polypeptides listed in tables 2 and/or 3, or stimulate or inhibit the expression of any of said polypeptides.

26. The proteins, compounds, kits, methods and uses substantially as herein before described, especially with reference to the foregoing examples.

***

Abstract

The present invention provides polypeptides which are up-regulated in pancreatic cancer and which can be used as markers for diagnosis of pancreatic cancer. The invention also provides an in vitro method for the diagnosis of pancreatic cancer and/or the susceptibility to pancreatic cancer comprising the steps of a) obtaining a biological sample; and b) detecting and/or measuring the increase of one or more polypeptides as disclosed herein. Furthermore, screening methods relating to inhibitors and antagonists of the specific polypeptides disclosed herein are provided.